

**SEARCH REQUEST FORM**

Scientific and Technical Information Center

Requester's Full Name: \_\_\_\_\_ Examiner #: \_\_\_\_\_ Date: \_\_\_\_\_  
 Art Unit: \_\_\_\_\_ Phone Number 30 \_\_\_\_\_ Serial Number: \_\_\_\_\_  
 Mail Box and Bldg/Room Location: \_\_\_\_\_ Results Format Preferred (circle): PAPER DISK E-MAIL

**If more than one search is submitted, please prioritize searches in order of need.**

\*\*\*\*\*

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: \_\_\_\_\_

Inventors (please provide full names): \_\_\_\_\_

Earliest Priority Filing Date: \_\_\_\_\_

*\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

\*\*\*\*\*

**STAFF USE ONLY****Type of Search****Vendors and cost where applicable**

Searcher: _____	NA Sequence (#) _____	STN _____
Searcher Phone #: _____	AA Sequence (#) _____	Dialog _____
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: _____	Bibliographic _____	Dr.Link _____
Date Completed: <u>4/10</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: _____	Fulltext _____	Sequence Systems _____
Clerical Prep Time: _____	Patent Family _____	WWW/Internet _____
Online Time: _____	Other _____	Other (specify) _____



GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: April 10, 2003, 11:52:51 ; Search time 30 Seconds  
(without alignments)  
1428.593 Million cell updates/sec

Title: US-09-720-469a-44

Perfect score: 208  
Sequence: 1 MKVLAALINGSVFLLLP.....VILADCGKIEVEKFAIAKE 208

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size : 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

SPREMBL\_21:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_protist:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	208	100.0	216	4	Q9BVK5
2	98	47.1	208	11	Q88541
3	98	47.1	216	11	Q9DCY1
4	37	17.8	203	3	Q01490
5	29	13.9	212	3	Q8X166
6	28	13.5	87	6	Q29278
7	28	13.5	214	3	Q94190
8	19	9.1	162	10	Q92T54
9	19	9.1	207	3	Q8X0S3
10	18	8.7	143	5	Q917V3
11	18	8.7	143	5	Q25093
12	18	8.7	220	5	Q9W227
13	18	8.7	220	5	Q44073
14	18	8.7	226	3	Q93826
15	17	8.2	167	5	Q15729
16	17	8.2	204	5	Q62190

17	16	7.7	197	5	Q9TW32	Q9TW32 dictyosteli
18	16	7.7	212	4	Q96CA2	Q96CA2 homo sapien
19	16	7.7	213	5	Q27774	Q27774 schistosoma
20	15	7.2	173	10	Q9FW22	Q9FW22 oryza sativ
21	15	7.2	177	4	Q43447	Q43447 homo sapien
22	15	7.2	177	11	Q9CC07	Q9CC07 mus musculu
23	15	7.2	183	5	Q9V9B9	Q9V9B9 drosophila
24	15	7.2	188	11	Q9D868	Q9D868 mus musculu
25	15	7.2	210	5	Q9U6U5	Q9U6U5 plasmodium
26	15	7.2	210	5	Q27716	Q27716 plasmodium
27	14	6.7	172	10	Q65104	Q65104 chlamydomon
28	14	6.7	213	5	Q26551	Q26551 schistosoma
29	13	6.2	87	11	Q9CWD4	Q9CWD4 rattus sp.
30	13	6.2	104	13	Q98UE5	Q98UE5 xenopus lae
31	13	6.2	165	3	Q9HRU2	Q9HRU2 magnaporthe
32	13	6.2	172	10	Q96417	Q96417 digitalis 1
33	13	6.2	179	5	Q26994	Q26994 toxoplasma
34	13	6.2	215	3	Q9HFU3	Q9HFU3 magnaporthe
35	13	6.2	234	10	Q9LY53	Q9LY53 arabidopsis
36	13	6.2	357	4	Q96DG9	Q96DG9 homo sapien
37	13	6.2	752	11	Q55035	Q55035 rattus norv
38	13	6.2	754	4	Q13427	Q13427 homo sapien
39	12	5.8	105	4	Q9BVG1	Q9BVG1 homo sapien
40	12	5.8	112	10	Q65191	Q65191 fucus distl
41	12	5.8	156	6	Q9MZD3	Q9MZD3 canis faml
42	12	5.8	160	10	Q9M530	Q9M530 euphorbia e
43	12	5.8	161	5	Q26565	Q26565 schistosoma
44	12	5.8	164	5	Q9XZ25	Q9XZ25 lumbricus r
45	12	5.8	164	11	Q9CWD5	Q9CWD5 mus musculu

## ALIGNMENTS

## RESULT 1

Q9BVK5 PRELIMINARY; PRT; 216 AA.  
ID Q9BVK5  
AC Q9BVK5;  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
DE Peptidylprolyl isomerase B (cyclophilin B).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Carnivora; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=SKIN;  
RA Strausberg R.;  
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=SKIN;  
RA Strausberg R.;  
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=PROSTATE;  
RA Strausberg R.;  
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
CC -! FUNCTION: PRASES ACCELERATE THE FOLDING OF PROTEINS (BY SIMILARITY).  
CC -! CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC  
CC PEPTIDE BONDS IN OLIGOPEPTIDES.  
CC -! SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PRASE FAMILY.  
DR EMBL: BC001125; AAH01125.1; -  
DR EMBL: BC008848; AAH08848.1; -  
DR EMBL: BC020800; AAH20800.1; -  
DR HSSP: P23284; ICYN.  
DR InterPro: IPR002130; CSA\_PRASE.  
DR Pfam: PF00160; pro\_isomerase 1.  
DR PRINTS: PR00153; CSAPISEMASE.

DR PROSITE: PS00170; CSA\_PPIASE\_1; 1.  
 DR PROSITE: PS00072; CSA\_PPIASE\_2; 1.  
 KW Isomerase; Rotomase.  
 SQ SEQUENCE 216 AA; 23742 MW; 2D0410A07AA9E420 CRC64;

Query Match 100.0%; Score 208; DB 4; Length 216;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
 Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MKLLAAALAGSVFLLLPSPADKKKGPVTVYKVFDLAIGEDVGRVIFGLFGKT 60  
 DB 9 MKLLAAALAGSVFLLLPSPADKKKGPVTVYKVFDLAIGEDVGRVIFGLFGKT 68  
 OY 61 VPKTVNFAALATGEGFGYKNSKFRVIRKDFMIOGDDFTRGDGTGKSTYGERPDENF 120  
 DB 69 VPKTVNFAALATGEGFGYKNSKFRVIRKDFMIOGDDFTRGDGTGKSTYGERPDENF 128  
 OY 121 KLKHYPGWSMANAGKDTNGSOFFITTVYKTAWLDEKHHVFGKYLEGMEYVRKVESTKTD 180  
 DB 129 KLKHYPGWSMANAGKDTNGSOFFITTVYKTAWLDEKHHVFGKYLEGMEYVRKVESTKTD 188  
 OY 181 SRDKPLKDVIIADCGKIEVEKPPAIAKE 208  
 DB 189 SRDKPLKDVIIADCGKIEVEKPPAIAKE 216

## RESULT 2

088541 PRELIMINARY; PRT; 208 AA.

AC 088541;  
 DT 01-NOV-1998 (TREMBLrel. 08, Created)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 DE Cyclophilin B.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=WISTAR-KYOTO; TISSUE=KIDNEY;  
 RA Kainer D.B., Doris P.A.;  
 RT "Cyclophilin B."  
 RL Submitted (JUN-1998) to the EMBL/Genbank/DBJ databases.  
 CC -1- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS (BY SIMILARITY).  
 CC -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.  
 CC -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.  
 DR EMBL; AF07125; AAC25590.1; -.  
 DR HSSP; P23284; ICYN.  
 DR InterPro: IPR002130; CSA\_PPIase.  
 DR Pfam: PF00160; pro\_isomerase; 1.  
 DR PRINTS; PR00153; CSAPPISMRASE.  
 DR PROSITE; PS00170; CSA\_PPIASE\_1; 1.  
 DR PROSITE; PS00072; CSA\_PPIASE\_2; 1.  
 KW Isomerase; Rotomase.  
 SQ SEQUENCE 208 AA; 22802 MW; 0240BFA7157218C CRC64;

Query Match 47.1%; Score 98; DB 11; Length 208;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-92;  
 Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 54 FGLFGKTVKTYDNFVALATGEGFGYKNSKFRVIRKDFMIOGDDFTRGDGTGKSTYGE 113  
 DB 54 FGLFGKTVKTYDNFVALATGEGFGYKNSKFRVIRKDFMIOGDDFTRGDGTGKSTYGE 113  
 OY 114 RPPDENFKLKHYPGWSMANAGKDTNGSOFFITTVYKT 151  
 DB 114 RPPDENFKLKHYPGWSMANAGKDTNGSOFFITTVYKT 151

## RESULT 3

09DCY1  
 ID 09DCY1 PRELIMINARY; PRT; 216 AA.

AC 09DCY1;  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Peptidylprolyl isomerase B.  
 GN PPIB.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=KIDNEY;  
 RX MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleschmann W., Gaasterland T., Glasl C., Kling B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Holtman M., Hume D.A., Kamya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitaker C., Willing L.,  
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,  
 RA Hayashizaki Y.,  
 RT "Functional annotation of a full-length mouse cDNA collection."  
 RL Nature 409:685-690(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=BREAST TUMOR;  
 RA Strausberg R.;  
 RL Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; AK002357; BAB22036.1; -.  
 DR EMBL; BC013061; AAH13061.1; -.  
 DR HSSP; P23284; ICYN.  
 DR MGD; MGI:97750; Ppib.  
 DR InterPro: IPR002130; CSA\_PPIase.  
 DR Pfam; PF00160; pro\_isomerase; 1.  
 DR PRINTS; PR00153; CSAPPISMRASE.  
 DR PROSITE; PS00170; CSA\_PPIASE\_1; 1.  
 DR PROSITE; PS00072; CSA\_PPIASE\_2; 1.  
 KW Isomerase.  
 SQ SEQUENCE 216 AA; 23713 MW; CE9DAD1544AE72FE CRC64;

Query Match 47.1%; Score 98; DB 11; Length 216;  
 Best Local Similarity 100.0%; Pred. No. 6.6e-92;  
 Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 54 FGLFGKTVKTYDNFVALATGEGFGYKNSKFRVIRKDFMIOGDDFTRGDGTGKSTYGE 113  
 DB 62 FGLFGKTVKTYDNFVALATGEGFGYKNSKFRVIRKDFMIOGDDFTRGDGTGKSTYGE 121  
 OY 114 RPPDENFKLKHYPGWSMANAGKDTNGSOFFITTVYKT 151  
 DB 122 RPPDENFKLKHYPGWSMANAGKDTNGSOFFITTVYKT 159

## RESULT 4

001490 PRELIMINARY; PRT; 203 AA.

ID 001490;  
 DT 01-NOV-1998 (TREMBLrel. 08, Created)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

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DE Peptidyl-prolyl cis-trans isomerase B precursor (EC 5.2.1.8) (PPIase)
GN (Cyclophilin B) (rotamase).
OS Orpinomyces sp. PC-2.
OC Eukaryota; Fungi; Chytridiomycota; Neocallimastixales;
OC Neocallimastixaceae; Orpinomyces.
OX NCBI_TaxID=50059;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 23-52.
RA MEDLINE=95223986; PubMed=7708690;
RX Chen H., Li X.-L., Ljungdahl L.G.;
RT "A cyclophilin from the polycentric anaerobic rumen fungus Orpinomyces
RT sp. strain PC-2 is highly homologous to vertebrate cyclophilin B.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:2587-2591(1995).
CC -1- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
CC -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -1- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
DR EMBL: U17900; AAD04195.1; -.
DR HSSP: P23284; ICYN.
DR InterPro: IPR002130; CSA_PPIase.
DR Pfam: PF00160; pro_isomerase.1.
DR PRINTS: PR00153; CSAPPISMASE.
DR PROSITE: PS00170; CSA_PPIASE_1; 1.
DR PROSITE: PS50072; CSA_PPIASE_2; 1.
KM Isomerase; rotamase; Signal; Cyclosporin; Endoplasmic reticulum.
FT CHAIN 1 203 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B.
FT BINDING 147 147 CSA (POTENTIAL).
FT SITE 200 203 PREVENT SECRETION FROM ER
FT (BY SIMILARITY).
SQ SEQUENCE 203 AA; 21969 MW; A5748C94305B8BE0 CRC64;

Query Match 17.8%; Score 37; DB 3; Length 203;
Best Local Similarity 100.0%; Pred. No. 1.8e-29;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 GYKNSKFRVIRKDFMIOGGDFTRGDTGKSIYGERF 115
DQ 73 GYKNSKFRVIRKDFMIOGGDFTRGDTGKSIYGERF 109
|||||
ID 08X166 PRELIMINARY; PRT; 212 AA.
AC 08X166;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Cyclophilin-like peptidyl prolyl cis-trans isomerase (EC
DE 5.2.1.8).
GN CYPB.
OS Aspergillus niger.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5061;
RN [1]
RP SEQUENCE FROM N.A.
RA Derx P.M.F., Madrid S.M.;
RT "The foldase Cyb is a component of the secretory pathway of
RT Aspergillus niger and contains the endoplasmic reticulum retention
RT signal HEEL.";
RL Mol. Gen. Genet. 266:537-545(2001).
DR EMBL: AY005867; AAF98447.1; -.
DR InterPro: IPR002130; CSA_PPIase.
DR InterPro: IPR000886; ER_target.
DR Pfam: PF00160; pro_isomerase.1.
DR PRINTS: PR00153; CSAPPISMASE.
DR PROSITE: PS00170; CSA_PPIASE_1; UNKNOWN_1.
DR PROSITE: PS50072; CSA_PPIASE_2; 1.
DR PROSITE: PS00014; ER_TARGET; UNKNOWN_1.

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KM Isomerase. 212 AA; 23302 MW; FA00BA7DIE50019C CRC64;
SQ SEQUENCE 212 AA; 23302 MW; FA00BA7DIE50019C CRC64;

Query Match 13.9%; Score 29; DB 3; Length 212;
Best Local Similarity 100.0%; Pred. No. 3e-21;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 FHRVIRKDFMIOGGDFTRGDTGKSIYGE 113
DQ 84 FHRVIRKDFMIOGGDFTRGDTGKSIYGE 112
|||||
ID 029278 PRELIMINARY; PRT; 87 AA.
AC 029278;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Cyclophilin B (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SMALL INTESTINE;
RX MEDLINE=96327607; PubMed=8672129;
RA Winteroe A.K., Fredholm M., Davies W.;
RT "Evaluation and characterization of a porcine small intestine cDNA
RT library.";
RL Mamm. Genome 7:509-517(1996).
DR EMBL: F14628; CAA23162.1; -.
DR HSSP: P23284; ICYN.
DR InterPro: IPR002130; CSA_PPIase.
DR Pfam: PF00160; pro_isomerase.1.
DR PRINTS: PR00153; CSAPPISMASE.
DR PROSITE: PS50072; CSA_PPIASE_2; 1.
FT NON_TER 1 1
FT NON_TER 87 87
SQ SEQUENCE 87 AA; 9551 MW; EB3EAB68ED630AE97 CRC64;

Query Match 13.5%; Score 28; DB 6; Length 87;
Best Local Similarity 100.0%; Pred. No. 1.3e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 153 WLDKHVFVGVKVLGMEVYKRVESTKTD 180
DQ 32 WLDKHVFVGVKVLGMEVYKRVESTKTD 59
|||||
ID 094190 PRELIMINARY; PRT; 214 AA.
AC 094190;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Cyclophilin B.
GN CYPB.
OS Emericella nidulans.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; Emericella.
OX NCBI_TaxID=162425;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99343878; PubMed=10413615;
RA Joseph J.D., Heitman J., Means A.R.;
RT "Molecular cloning and characterization of Aspergillus nidulans
RT cyclophilin B.";
RL Fungal Genet. Biol. 27:55-66(1999).
CC -1- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS (BY
CC SIMILARITY).

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RESULT 9	
Q8X053	
ID Q8X053	PRELIMINARY;
AC Q8X053	PRT; 207 AA.
DT 01-MAR-2002	(TREMBlrel. 20, Created)
DT 01-MAR-2002	(TREMBlrel. 20, Last sequence update)

RESULT 10	Q917V3	PRELIMINARY:	PRT:	120 AA.
ID	Q917V3			
AC	Q917V3			
DT	01-MAR-2001 (TREMBLrel. 16, Created)			
DI	01-MAR-2001 (TREMBLrel. 16, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	CG2852 protein.			
GN	CG2852.			
OS	Drosophila melanogaster (Fruit fly).			
OCC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;			
OCC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
OCC	Ephyridiidae; Drosophilidae; Drosophila.			
OX	NCBI_TaxID=7227;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BERKELEY.			
RX	MEDLINE=20196006; PubMed=10731132;			
	Adams M.D., Gelniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amaralides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blaise R.G., Champagne M., Pfeiffer B.D., Wan K.F., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Famnoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P., Buttis K.C., Busam D.A., Butler H., Cadieu L.E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablos R., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durlin K.J., Evangelista C.C., Ferraz C., Fertler S., Fleischmann W., Foster C., Garskeian A.E., Garg N.S., Gelbart W.M., Glaser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harey D., Heiman T.J., Hernandez J.B., Houck J., Hostin D., Houston K.A., Howard T.J., Hernandez J., Ibergwam C., Jajali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Laako P., Lai Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,			



KW Isomerase: Rotamase.  
SQ SEQUENCE 205 AA; 22199 MW; A9CEFE88B1CC813F7 CRC64;

Query Match 8.7%; Score 18; DB 5; Length 205;  
Best Local Similarity 100.0%; Pred. No. 5,4e-10;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 131 SMANAGKDTNGSQFFITTT 148  
DB 124 SMANAGKDTNGSQFFITTT 141

## RESULT 13

ID 044073 PRELIMINARY; PRT; 220 AA.  
AC 044073;  
DT 01-JUN-1998 (TREMBlrel. 06, Created)  
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)  
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
DE Peptidyl-prolyl cis-trans isomerase G precursor (EC 5.2.1.8) (PPIase)  
DE (Rotamase) (Cyclophilin G) (P27).  
OS Tachypleus tridentatus (Japanese horseshoe crab).  
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;  
OC Limulidae; Tachypleus.  
OX NCBI\_Taxid-6853;

RN [1]  
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RC TISSUE-HEMOCYTE;  
RX MEDLINE-98019238; PubMed-9353327;  
RA Takaki Y., Muta T., Iwanaga S.;  
RT "A peptidyl-prolyl cis/trans-isomerase (cyclophilin G) in regulated secretory granules."  
RL J. Biol. Chem. 272:28615-28621(1997).  
CC -1- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS. MAY PLAY A ROLE IN MAINTAINING THE CONFORMATIONAL INTEGRITY OF STORED GRANULAR PROTEINS.  
CC -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.  
CC -1- ENZYME REGULATION: INHIBITED BY CYCLOSPORIN A (CSA).  
CC -1- TISSUE SPECIFICITY: HEMOCYTE LARGE SECRETORY GRANULES.  
CC -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.  
DR EMBL; AB002814; BAA33764.1; -.  
DR HSSP; P23284; ICYN.  
DR InterPro; IPR002130; CSA\_PPIase.  
DR Pfam; PF00160; pro\_isomerase; 1.  
DR PRINTS; PR00153; CSA\_PPIASERASE.  
DR PROSITE; PS00170; CSA\_PPIASE\_1; 1.  
DR PROSITE; PS50072; CSA\_PPIASE\_2; 1.  
KW Cyclosporin; Isomerase; Rotamase; Signal; Multigene family.  
FT SIGNAL 1 23  
FT CHAIN 24 220  
SQ SEQUENCE 220 AA; 24198 MW; 728CB63EBB821C68 CRC64;

Query Match 8.7%; Score 18; DB 5; Length 220;  
Best Local Similarity 100.0%; Pred. No. 5,7e-10;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 109 SIYGERFPDENFKLKHG 126  
DB 117 SIYGERFPDENFKLKHG 124

## RESULT 14

ID 093826 PRELIMINARY; PRT; 226 AA.  
AC 093826;  
DT 01-MAY-1999 (TREMBlrel. 10, Created)  
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)  
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
DE Cyclophilin  
OS Arthroderma benhamiae.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
OC Onygenales; Arthrodermataceae; Arthroderma.

OX NCBI\_Taxid-63400;

RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-VUT-77011;  
RX MEDLINE-20174741; PubMed-10711599;  
RA Kano R., Nakamura Y., Matanabe S., Tsujimoto H., Hasegawa A.;  
RT "Characterization of the cyclophilin of Trichophyton mentagrophytes."  
RL Microbiol. Immunol. 44:51-56(2000).  
CC -1- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS (BY SIMILARITY).  
CC -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.  
CC -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.  
DR EMBL; AB019518; BAA34384.1; -.  
DR HSSP; P23284; ICYN.  
DR InterPro; IPR002130; CSA\_PPIase.  
DR Pfam; PF00160; pro\_isomerase; 1.  
DR PRINTS; PR00153; CSA\_PPIASERASE.  
DR PROSITE; PS00170; CSA\_PPIASE\_1; 1.  
DR PROSITE; PS50072; CSA\_PPIASE\_2; 1.  
KW Isomerase; Rotamase.  
SQ SEQUENCE 226 AA; 24764 MW; 4D563B4943B27F12 CRC64;

Query Match 8.7%; Score 18; DB 3; Length 226;  
Best Local Similarity 100.0%; Pred. No. 5,9e-10;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 131 SMANAGKDTNGSQFFITTT 148  
DB 130 SMANAGKDTNGSQFFITTT 147

## RESULT 15

ID 015729 PRELIMINARY; PRT; 167 AA.  
AC 015729;  
DT 01-JAN-1998 (TREMBlrel. 05, Created)  
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)  
DE 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
DE Cyclophilin.  
GN CYPL.  
OS Entamoeba histolytica.  
OC Eukaryota; Entamoebidae; Entamoeba.  
OX NCBI\_Taxid-5759;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-HMI-1MSS;  
RX MEDLINE-20243663; PubMed-10779598;  
RA Ostoa-Saloma P., Carrero J.C., Petrossian P., Herion P., Landa A., Lacleite J.P.;  
RT "Cloning, characterization and functional expression of a cyclophilin from Entamoeba histolytica."  
RL Mol. Biochem. Parasitol. 107:219-225(2000).  
CC -1- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS (BY SIMILARITY).  
CC -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.  
CC -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.  
DR EMBL; AF017993; AAB86601.1; -.  
DR HSSP; P05092; ZCPL.  
DR InterPro; IPR002130; CSA\_PPIase.  
DR Pfam; PF00160; pro\_isomerase; 1.  
DR PRINTS; PR00153; CSA\_PPIASERASE.  
DR PROSITE; PS00170; CSA\_PPIASE\_1; 1.  
DR PROSITE; PS50072; CSA\_PPIASE\_2; 1.  
KW Isomerase; Rotamase.  
SQ SEQUENCE 167 AA; 18139 MW; DBA23FE5BB3290B2 CRC64;

Query Match 8.2%; Score 17; DB 5; Length 167;  
Best Local Similarity 100.0%; Pred. No. 4,6e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 85 FHRVINDPMIGGDFTR 101



Thu Apr 10 14:25:11 2003

us-09-720-469a-44.rspt

Db 55 FHRVKKDFMIGSDPTR 71

Search completed: April 10, 2003, 11:55:13  
Job time : 33 secs



GenCore version 5.1.4.p5 4578  
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OM protein - protein search, using sw model

Run on: April 10, 2003, 11:51:46 ; Search time 36 Seconds

(without alignments)  
769.892 Million cell updates/sec

Title: US-09-720-469a-44

Perfect score: 208

Sequence: 1 MKVLLAALAGSVFLLP.....VITADCGKIEVKEPAFAAKE 208

Scoring table:

OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 908470 seqs, 133250620 residues

Word size : 0

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

A.Geneseq\_101002:\*

- 1: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:\*
- 2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*
- 3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:\*
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- 5: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:\*
- 6: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:\*
- 7: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:\*
- 8: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:\*
- 9: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:\*
- 10: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:\*
- 11: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:\*
- 12: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:\*
- 13: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:\*
- 14: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:\*
- 15: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:\*
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- 18: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:\*
- 19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:\*
- 20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:\*
- 21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:\*
- 22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*
- 23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	208	100.0	216	22	AA873301	Human cyclophilin
2	208	100.0	291	21	AA843878	Human cancer assoc
3	208	100.0	291	23	ABP41842	Human ovarian anti
4	203	97.6	211	22	AA873302	Human cyclophilin
5	183	88.0	183	22	AA65273	Haematopoietic ste
6	137	65.9	166	21	AA600090	Haematopoietic ste
7	98	47.1	183	22	AA65274	Human secreted pro
8	64	30.8	64	23	AA09181	Haematopoietic ste
9	29	13.9	212	21	AA92048	Partial human pert
10	22	10.6	83	22	AA24287	A. human peptidyl- Human EST encoded

11	18	8.7	120	22	AB867378	Drosophila melanog
12	18	8.7	205	22	AB859287	Drosophila melanog
13	16	7.7	180	19	AA80784	D. discoideum cycl
14	16	7.7	185	22	AA65277	Haematopoietic ste
15	16	7.7	185	22	AA65278	Haematopoietic ste
16	16	7.7	212	14	AA82353	Cyclophilin C. Mu
17	15	7.2	58	22	ABG12991	Novel human diagno
18	15	7.2	58	22	ABG29318	Novel human diagno
19	15	7.2	183	21	AA856701	Human prostate can
20	15	7.2	183	22	AB866236	Drosophila melanog
21	15	7.2	193	23	ABP42003	Human ovarian anti
22	15	7.2	214	22	ABG23479	Novel human diagno
23	15	7.2	250	22	ABG23480	Novel human diagno
24	13	6.2	125	21	AA618027	Arabidopsis thalia
25	13	6.2	228	21	AA618026	Arabidopsis thalia
26	13	6.2	236	21	AA618025	Arabidopsis thalia
27	13	6.2	737	22	ABG10283	Novel human diagno
28	13	6.2	754	23	AAE24596	Human SR-cyp prote
29	12	5.8	106	22	ABG27275	Novel human diagno
30	12	5.8	114	22	AA864736	Gene 14 human secr
31	12	5.8	145	12	AA810763	Porcine peptidyl-p
32	12	5.8	145	16	AA872917	Porcine peptidyl p
33	12	5.8	145	16	AA872961	Porcine peptidyl p
34	12	5.8	152	21	AA608983	Arabidopsis thalia
35	12	5.8	162	21	AA644157	Arabidopsis thalia
36	12	5.8	163	12	AA813726	Bovine cyclophilin
37	12	5.8	163	22	AA65276	Haematopoietic ste
38	12	5.8	164	10	AA890431	Cyclophilin. Homo
39	12	5.8	164	22	AA65275	Haematopoietic ste
40	12	5.8	165	19	AA656028	Calcineurin protei
41	12	5.8	165	21	AA603831	Human secreted pro
42	12	5.8	165	22	AA601195	Human cyclophilin
43	12	5.8	169	23	ABP42929	Human ovarian anti
44	12	5.8	176	21	AA64156	Arabidopsis thalia
45	12	5.8	184	23	ABP41129	Human ovarian anti

#### ALIGNMENTS

RESULT 1  
AA873301  
ID AAB73301 standard; protein: 216 AA.  
XX  
AC AAB73301;  
XX  
DT 22-MAY-2001 (first entry)  
XX  
DE Human cyclophilin B (Cyph).  
KW Human cyclophilin B; Cyph; prolactin-binding; growth hormone-binding;  
KW somatolactogenic function modulator; immunosuppression; short stature;  
KW muscle wasting; osteoporosis; HIV infection; breast cancer;  
KW prostate cancer; gigantism; acromegaly; hypoprolactinemia.  
XX  
OS Homo sapiens.  
XX  
PN WO200113113-A1.  
XX  
PD 22-FEB-2001.  
XX  
PF 10-AUG-2000; 2000WO-US21789.  
XX  
PR 19-AUG-1999; 99US-0149752.  
XX  
PA (UYPE-) UNIV PENNSYLVANIA.  
XX  
PI Clevenger CV, Ryczyn MA.  
XX  
DR WPI; 2001-211249/21.  
XX  
PT Novel composition for modulating somatolactogenic function, comprises cyclophilin B, its mutant or an inhibitor of interaction of cyclophilin

PT B with somatotactogenic hormone -  
 XX  
 PS Claim 1; Page 17-18; 21pp; English.  
 CC The invention relates to a composition for modulating somatotactogenic  
 CC function, comprising cyclophilin B (CypB), a mutant of cyclophilin B  
 CC (particularly a CypB mutant in which residues 2-12 of the mature protein  
 CC are absent) or an inhibitor of the interaction of cyclophilin B with a  
 CC somatotactogenic hormone (e.g., prolactin, growth hormone). The invention  
 CC also relates to a method of identifying inhibitors of somatotactogenic  
 CC functions using CypB and a somatotactogenic hormone, and a method for  
 CC diagnosing diseases associated with abnormal somatotactogenic functions  
 CC by assessing CypB levels in a sample from a patient. Cyclophilin B is  
 CC useful for augmenting somatotactogenic function in the animal, and  
 CC cyclophilin B mutant or a composition comprising an inhibitor of the  
 CC interaction of cyclophilin B with a somatotactogenic hormone, is useful  
 CC for inhibiting somatotactogenic function in the animal. A composition  
 CC comprising cyclophilin B is useful in the treatment of immunosuppression,  
 CC in the treatment of short stature, muscle wasting and osteoporosis. A  
 CC composition comprising cyclophilin B mutant or a composition comprising  
 CC an inhibitor of the interaction of cyclophilin B with a somatotactogenic  
 CC hormone, is useful for treating HIV infection, breast and prostate  
 CC cancer, gigantism/acromegaly, and hyperprolactinaemia. The present  
 CC sequence represents human cyclophilin B.  
 XX  
 S0 Sequence 216 AA:  
 Query Match 100.0%; Score 208; DB 22; Length 216;  
 Best Local Similarity 100.0%; Pred. No. 4,9e-194;  
 Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MKVLLAALIAAGVFLLPGPSADDEKKKGPVKVYFDLRIGDEDEGRVIFGLFGKT 60  
 DB 9 MKVLLAALIAAGVFLLPGPSADDEKKKGPVKVYFDLRIGDEDEGRVIFGLFGKT 68  
 QY 61 VKPTVDNFVALATGEGKGYKNSKFRHRYIKDPMIOGDFTRDGDYGKSIYGERPPDENF 120  
 DB 69 VKPTVDNFVALATGEGKGYKNSKFRHRYIKDPMIOGDFTRDGDYGKSIYGERPPDENF 128  
 QY 121 KLRHVGPGVSMANAGKDTNGSQFFITTYKTMLDGKHVFEKVLLEGMEVVKVVESTKTD 180  
 DB 129 KLRHVGPGVSMANAGKDTNGSQFFITTYKTMLDGKHVFEKVLLEGMEVVKVVESTKTD 188  
 QY 181 SDRKPLKDVITADCGKIEVEKFFAIAKE 208  
 DB 189 SDRKPLKDVITADCGKIEVEKFFAIAKE 216  
 RESULT 2  
 AAB43878 standard; Protein; 291 AA.  
 XX  
 AC AAB43878;  
 XX  
 DT 08-FEB-2001 (first entry)  
 DE Human cancer associated protein sequence SEQ ID NO:1323.  
 XX  
 KW Human; cancer associated gene; cancer antigen; detection; cancer;  
 KW diagnosis; cytostatic; proliferative; vulnereary; immunomodulator;  
 KW antidiabetic; antiaesthetic; antirheumatic; antiarthritic; antiviral;  
 KW antinflammatory; antihypertensive; antiallergic; antibacterial; cardiac;  
 KW dermatological; neuroprotective; thrombolytic; coagulant; nootropic;  
 KW vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation;  
 KW immune disorder; haematopoietic cell disorder; autoimmune disorder;  
 KW allergic reaction; graft versus host disease; organ rejection;  
 KW haemostatic; thrombolytic; cardiovascular disorder; infection;  
 KW neurological disease; drug screening.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX WO20005350-A1.  
 XX

PD 21-SEP-2000.  
 XX  
 XX 08-MAR-2000; 2000WO-US05882.  
 XX  
 PR 12-MAR-1999; 99US-0124270.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Rosen CA, Ruben SM;  
 XX  
 DR WPI: 2000-587533/55.  
 DR N-PSDB: AAC78087.  
 PR Novel isolated nucleic acids comprising sequences encoding peptides  
 PT useful for treating or diagnosing e.g. cancer -  
 XX  
 XX Claim 11; Page 1974-1975; 2352pp; English.  
 PS  
 CC AAC77607 to AAC78448 encode the human cancer associated proteins given  
 CC in AAB43398 to AAB44239. The proteins can have activities based on the  
 CC tissues and cells the genes are expressed in. Example of activities  
 CC include: cytostatic; proliferative; vulnereary; immunomodulator;  
 CC antidiabetic; antiaesthetic; antirheumatic; antiarthritic;  
 CC antinflammatory; antihypertensive; antiallergic; antibacterial; antiviral;  
 CC dermatological; neuroprotective; cardiac; thrombolytic; coagulant;  
 CC vasotropic; antipsoriatic; antiangiogenic;  
 CC polynucleotides and polypeptides can be used for preventing, treating or  
 CC ameliorating medical conditions and diagnosing pathological conditions.  
 CC Polynucleotides, polypeptides, antibodies, agonists and antagonists from  
 CC the present invention may be used to treat immune disorders by activating  
 CC or inhibiting the proliferation, differentiation or mobilisation of  
 CC immune cells, to treat disorders of haematopoietic cells, autoimmune  
 CC disorders, allergic reactions, graft versus host disease and organ  
 CC rejection, modulate haemostatic or thrombolytic activity, modulate  
 CC inflammation, cancers, cardiovascular disorders, neurological disease and  
 CC bacterial or viral infections. The peptides, nucleotides, antibodies and  
 CC agonists and antagonists may be also be used in drug screens. AAC78449 to  
 CC AAC78457 and AAB44240 represent sequences used in the exemplification of  
 CC the present invention.  
 XX  
 S0 Sequence 291 AA:  
 Query Match 100.0%; Score 208; DB 21; Length 291;  
 Best Local Similarity 100.0%; Pred. No. 6,4e-194;  
 Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MKVLLAALIAAGVFLLPGPSADDEKKKGPVKVYFDLRIGDEDEGRVIFGLFGKT 60  
 DB 84 MKVLLAALIAAGVFLLPGPSADDEKKKGPVKVYFDLRIGDEDEGRVIFGLFGKT 143  
 QY 61 VKPTVDNFVALATGEGKGYKNSKFRHRYIKDPMIOGDFTRDGDYGKSIYGERPPDENF 120  
 DB 144 VKPTVDNFVALATGEGKGYKNSKFRHRYIKDPMIOGDFTRDGDYGKSIYGERPPDENF 203  
 QY 121 KLRHVGPGVSMANAGKDTNGSQFFITTYKTMLDGKHVFEKVLLEGMEVVKVVESTKTD 180  
 DB 204 KLRHVGPGVSMANAGKDTNGSQFFITTYKTMLDGKHVFEKVLLEGMEVVKVVESTKTD 263  
 QY 181 SDRKPLKDVITADCGKIEVEKFFAIAKE 208  
 DB 264 SDRKPLKDVITADCGKIEVEKFFAIAKE 291  
 RESULT 3  
 ABA1842 standard; Protein; 291 AA.  
 ID ABA1842  
 XX  
 AC ABA1842;  
 XX  
 DT 22-AUG-2002 (first entry)  
 DE Human ovarian antigen HTFML39, SEQ ID NO:2974.  
 XX

Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;  
 ovarian cancer; breast cancer; tumour; reproductive system disorder;  
 infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;  
 PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;  
 inflammatory condition; immune disorder; blood disorder;  
 cardiovascular disorder; respiratory disorder; neurological disorder;  
 gastrointestinal disorder; urinary system disorder; drug screening;  
 gene therapy; chromosome mapping; forensic analysis;  
 antibody preparation; cytostatic; immunomodulatory; neuroprotective;  
 antiinflammatory; gynecological; reproductive.

XX Homo sapiens.  
 OS  
 PN WO200200677-A1.  
 PD 03-JAN-2002.  
 XX  
 PF 07-JUN-2001; 2001WO-US18569.  
 XX  
 PR 07-JUN-2000; 2000US-209467P.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PI Birse CE, Rosen CA;  
 DR WPI: 2002-147878/19.  
 DR N-PSDB: ABO54919.  
 XX  
 PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,  
 useful in the prevention, treatment and diagnosis of cancer (e.g.  
 ovarian cancer), immune disorders, cardiovascular disorders and  
 neurological diseases -

PS  
 XX Claim 11: SEQ ID NO 2974; 2972pp: English.

CC The invention relates to 2175 novel human ovarian antigens (ABP41054-  
 CC ABP4328) and to cDNAs encoding them (ABO54131-ABO56305), and also  
 CC encompasses polypeptides 90% identical and polynucleotides 95% identical  
 CC to the sequences of the invention. The invention additionally relates to  
 CC recombinant vectors and host cells comprising human ovarian antigen  
 CC polynucleotides, antibodies against human ovarian antigen  
 CC of ovarian antigen polynucleotides and polypeptides in diagnosing,  
 CC treating, prognosing or preventing various ovarian and/or breast-related  
 CC disorders. Such conditions include ovarian cancer and breast cancer, and  
 CC metastatic tumours of ovarian or breast origin, reproductive system  
 CC disorders (e.g., infertility, disorders of pregnancy, anovulation,  
 CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhea), endocrine  
 CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic  
 CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and  
 CC vaginitis), immune disorders (e.g., congenital and acquired  
 CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),  
 CC blood-related disorders (e.g., anaemia), cardiovascular disorders,  
 CC respiratory disorders, neurological disorders, gastrointestinal disorders  
 CC and urinary system disorders. Ovarian antigen polypeptides and  
 CC polynucleotides may also be used in screening for compounds and  
 CC modulate ovarian antigen expression or activity. The polynucleotides may  
 CC further be used for gene therapy, chromosome mapping, in the  
 CC identification of individuals and in forensic analysis, and the  
 CC polypeptides may be used as food additives or to prepare antibodies  
 CC useful in disease diagnosis, drug targeting and phenotyping. The present  
 CC sequence represents a human ovarian antigen of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX  
 SO Sequence 291 AA:

Query Match 100.0%; Score 208; DB 23; Length 291;  
 Best Local Similarity 100.0%; Pred. No. 6,4e-194;  
 Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKVLLAALINGSVFELLPGPSAADEKKKGRVYKVFYDNLIGDEDEGVRVIFGLFGKT 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 84 MKVLLAALINGSVFELLPGPSAADEKKKGRVYKVFYDNLIGDEDEGVRVIFGLFGKT 143  
 QY 61 VPKTVDFNVALATGEKGFYKNSKFRHYIKDFMIQGGDFTRGDSGTGKSIYGERFPDENF 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 144 VPKTVDFNVALATGEKGFYKNSKFRHYIKDFMIQGGDFTRGDSGTGKSIYGERFPDENF 203  
 QY 121 KLKHGPGWVMANNGKPTNSOFFITTVKTAAMDGKRVYGVKYLEGMEVVRKVESTKT 180  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 204 KLKHGPGWVMANNGKPTNSOFFITTVKTAAMDGKRVYGVKYLEGMEVVRKVESTKT 263  
 QY 181 SRDRPLKDVIIADCGKIEVEKPAFAKE 208  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 264 SRDRPLKDVIIADCGKIEVEKPAFAKE 291

RESULT 4  
 AAB73302  
 ID AAB73302 standard; protein; 211 AA.  
 XX  
 AC AAB73302;  
 XX  
 DT 22-MAY-2001 (first entry)  
 XX  
 DE Human cyclophilin B (Cyb) C-terminal deletion mutant, Cyb-ATAKE.  
 XX  
 KW Human cyclophilin B; Cyb; prolactin-binding; growth hormone-binding;  
 KW somatolactogenic function modulator; immunosuppression; short stature;  
 KW muscle wasting; osteoporosis; HIV infection; breast cancer;  
 KW prostate cancer; gigantism; acromegaly; hyperprolactinaemia;  
 KW C-terminal deletion mutant; mutin.

XX  
 OS Homo sapiens.  
 XX  
 PN WO200113113-A1.  
 PD 22-FEB-2001.  
 XX  
 PF 10-AUG-2000; 2000WO-US21789.  
 XX  
 PR 19-AUG-1999; 99US-0149752.  
 XX  
 PA (UYPE-) UNIV PENNSYLVANIA.  
 XX  
 PI Clevenger CV, Ryczyn MA;  
 DR WPI: 2001-211249/21.  
 XX  
 PT Novel composition for modulating somatolactogenic function, comprises  
 PT cyclophilin B, its mutant or an inhibitor of interaction of cyclophilin  
 PT B with somatolactogenic hormone -

XX  
 PS Disclosure; Page -: 21pp: English.

CC The invention relates to a composition for modulating somatolactogenic  
 CC function, comprising cyclophilin B (Cyb), a mutant of cyclophilin B  
 CC (particularly a Cyb mutant in which residues 2-12 of the mature protein  
 CC are absent) or an inhibitor of the interaction of cyclophilin B with a  
 CC somatolactogenic hormone (e.g., prolactin, growth hormone). The invention  
 CC also relates to a method of identifying inhibitors of somatolactogenic  
 CC functions using Cyb and a somatolactogenic hormone, and a method for  
 CC diagnosing diseases associated with abnormal somatolactogenic functions  
 CC by assessing Cyb levels in a sample from a patient. Cyclophilin B is  
 CC useful for augmenting somatolactogenic function in the animal, and  
 CC cyclophilin B mutant or a composition comprising an inhibitor of the  
 CC interaction of cyclophilin B with a somatolactogenic hormone, is useful  
 CC for inhibiting somatolactogenic function in the animal. A composition  
 CC comprising cyclophilin B is useful in the treatment of immunosuppression,  
 CC in the treatment of short stature, muscle wasting and osteoporosis. A  
 CC composition comprising cyclophilin B mutant or a composition comprising  
 CC an inhibitor of the interaction of cyclophilin B with a somatolactogenic  
 CC hormone, is useful for treating HIV infection, breast and prostate  
 CC cancer, gigantism/acromegaly, and hyperprolactinaemia. The present  
 CC sequence represents a human cyclophilin B C-terminal mutant, Cyb-ATAKE.

CC Note: The present sequence is not shown in the specification, but  
CC is derived from the wild-type Cypb sequence shown on pages 17-18.

XX Sequence 211 AA;

Query Match 97.6%; Score 203; DB 22; Length 211;

Best Local Similarity 100.0%; Pred. No. 3.5e-189; Indels 0; Gaps 0;

Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKVLLAALIASGVFELLPGPSADEKKKGKPVYKVFYDLRIGDEVDGRIYFGLFGKT 60  
DB 9 MKVLLAALIASGVFELLPGPSADEKKKGKPVYKVFYDLRIGDEVDGRIYFGLFGKT 68  
QY 61 VKPTVDNFVALATGEGKGYKNSKFRHYIKDFMIOGDFTRDGTGKSIYGERPPDENF 120  
DB 69 VKPTVDNFVALATGEGKGYKNSKFRHYIKDFMIOGDFTRDGTGKSIYGERPPDENF 128  
QY 121 KKHVYGPVSMANAGKDTNGSQFFITTYKTAMLGDKHVFEGKVLGEGMEVAKVESTKT 180  
DB 129 KKHVYGPVSMANAGKDTNGSQFFITTYKTAMLGDKHVFEGKVLGEGMEVAKVESTKT 188  
QY 181 SRDKPLKDYIADCGKIEVEKPF 203  
DB 189 SRDKPLKDYIADCGKIEVEKPF 211

# RESULT 5

AAG65273  
ID AAC65273 standard; protein: 183 AA.

XX AAC65273;

DT 20-NOV-2001 (first entry)

XX Haematopoietic stem cell proliferation agent related human protein #1.

XX Haematopoietic stem cell proliferation agent; cyclophilin;

KW dyshaemopoiesis; cancer; human; mouse.

XX Homo sapiens.

PN JP2001163798-A.

PD 19-JUN-2001.

XX 03-DEC-1999; 99JP-0345542.

XX 03-DEC-1999; 99JP-0345542.

PA (KANF ) KANEKA CORP.

DR WPI: 2001-592517/67.

XX Proliferation agent for haematopoietic stem cell containing cyclophilin

PS Claim 2; Page 13-14; 19pp; Japanese.

XX The present invention provides a proliferation agent for haematopoietic  
CC stem cells, which contains cyclophilin. This may be used in the treatment  
CC of dyshaemopoiesis in radiotherapy and chemotherapy of various  
CC haematopoietic organ diseases and cancers. The present sequence is a  
CC human protein described in the exemplification of the invention.

XX Sequence 183 AA;

Query Match 88.0%; Score 183; DB 22; Length 183;

Best Local Similarity 100.0%; Pred. No. 8.8e-170; Indels 0; Gaps 0;

Matches 183; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 DEKKKPKVTVKVFYDLRIGDEVDGRIYFGLFGKTVPKVDNFVALATGEGKGYKNSKF 85  
DB 1 DEKKKPKVTVKVFYDLRIGDEVDGRIYFGLFGKTVPKVDNFVALATGEGKGYKNSKF 60

QY 86 HRVTKDFMIOGDFTRDGTGKSIYGERPPDENFKLKHVYGPVSMANAGKDTNGSQFF 145

DB 61 HRVTKDFMIOGDFTRDGTGKSIYGERPPDENFKLKHVYGPVSMANAGKDTNGSQFF 120

QY 146 ITTYKTAMLGDKHVFEGKVLGEGMEVAKVESTKTSDRDKPLKDYIADCGKIEVEKPPAI 205

DB 121 ITTYKTAMLGDKHVFEGKVLGEGMEVAKVESTKTSDRDKPLKDYIADCGKIEVEKPPAI 180

QY 206 AKE 208

DB 181 AKE 183

# RESULT 6

AAG00090  
ID AAC00090 standard; protein: 166 AA.

XX AAG00090;

DT 06-OCT-2000 (first entry)

XX Human secreted protein, SEQ ID NO: 4171.

XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;  
KW gene therapy; chromosome mapping.

XX Homo sapiens.

PN EP1033401-A2.

PD 06-SEP-2000.

XX 21-FEB-2000; 2000EP-0200610.

XX 26-FEB-1999; 99US-0122487.

PA (GEST ) GENSET.

PI Dumas Milne Edwards J, Duclert A, Giordano J;

DR WPI: 2000-500381/45.

XX N-PSDB; AAC00096.

XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for  
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for  
PT diagnostic, forensic, gene therapy and chromosome mapping procedures -  
PS Claim 13; SEQ ID 4171; 71pp + CD-ROM; English.

XX The present sequence is a polypeptide encoded by one of a large number  
CC of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs  
CC were prepared from total human RNAs or polyA+ RNAs derived from 30  
CC different tissues. EST sequences usually correspond mainly to the 3'  
CC untranslated region (UTR) of the mRNA because they are often obtained  
CC from oligo-dT primed cDNA libraries. Such ESTs are not well suited for  
CC isolating cDNA sequences derived from the 5' ends of mRNAs and even in  
CC those cases where longer cDNA sequences have been obtained, the full 5'  
CC UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5'  
CC ends and can therefore be used to obtain full length cDNAs and genomic  
CC DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and  
CC chromosome mapping procedures. They are used to obtain upstream  
CC regulatory sequences and to design expression and secretion vectors.

XX Sequence 166 AA;

Query Match 65.9%; Score 137; DB 21; Length 166;

Best Local Similarity 100.0%; Pred. No. 4.5e-125; Indels 0; Gaps 0;

Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKVLLAALIASGVFELLPGPSADEKKKGKPVYKVFYDLRIGDEVDGRIYFGLFGKT 60  
DB 9 MKVLLAALIASGVFELLPGPSADEKKKGKPVYKVFYDLRIGDEVDGRIYFGLFGKT 68

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QY 61 VPKTVDNFVALATGEGKGFYKNSKFRHVITKDFMIOGSDFTRGDGTGKSTYGERFPDENF 120
DB 69 VPKTVDNFVALATGEGKGFYKNSKFRHVITKDFMIOGSDFTRGDGTGKSTYGERFPDENF 128
QY 121 KLKHGPGWVSMANACK 137
DB 129 KLKHGPGWVSMANACK 145

RESULT 7
AAG5274
ID AAG5274 standard; protein; 183 AA.
AC AAG5274;
DT 20-NOV-2001 (first entry)
XX
DE Haematopoietic stem cell proliferation agent related murine protein #1.
XX
KW Haematopoietic stem cell proliferation agent; cyclophilin;
KW dyshaemopoiesis; cancer; human; mouse.
XX
OS Mus sp.
XX
PN JP2001163798-A.
XX
PD 19-JUN-2001.
XX
PF 03-DEC-1999; 99JP-0345542.
XX
PR 03-DEC-1999; 99JP-0345542.
XX
PA (KANF ) KANEKA CORP.
XX
DR MPI; 2001-592517/67.
XX
PT Proliferation agent for haematopoietic stem cell containing cyclophilin
PT
PS Claim 3; Page 14; 19pp; Japanese.
XX
CC The present invention provides a proliferation agent for haematopoietic
CC stem cells, which contains cyclophilin. This may be used in the treatment
CC of dyshaemopoiesis in radiotherapy and chemotherapy of various
CC haematopoietic organ diseases and cancers. The present sequence is a
CC murine protein described in the exemplification of the invention.
XX
SQ Sequence 183 AA;
Query Match 47.18; Score 98; DB 22; Length 183;
Best Local Similarity 100.0%; Pred. No. 4.2e-87;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 54 FGLGKTVPKTVDNFVALATGEGKGFYKNSKFRHVITKDFMIOGSDFTRGDGTGKSTYGE 113
DB 29 FGLGKTVPKTVDNFVALATGEGKGFYKNSKFRHVITKDFMIOGSDFTRGDGTGKSTYGE 88
QY 114 RFPDENFKLKHGPGWVSMANACKDTNGSQFFITTVKT 151
DB 89 RFPDENFKLKHGPGWVSMANACKDTNGSQFFITTVKT 126

RESULT 8
AAG9181
ID AAG9181 standard; Protein; 64 AA.
AC AAG9181;
DT 24-SEP-2002 (first entry)
XX
DE Partial human perturbation F802.
XX

```

```

KW Retinoic acid pathway; RA; retinoid; Lung cancer;
KW Kaposi's sarcoma; breast cancer; pancreatic cancer; neuroblastoma;
KW renal cancer; ovarian cancer; dermatitis; hyperkeratosis; eczema;
KW Darier's disease; Reiter's disease; psoriasis; gene therapy; F797;
KW acute promyelocytic leukaemia; APL; Perturbagen; R3; F802; F820;
KW yeast two-hybrid assay; PAT1; kinesin light chain-related protein;
KW human.
XX
OS Homo sapiens.
XX
PN WO200240719-A2.
XX
PD 23-MAY-2002.
XX
PF 17-NOV-2001; 2001WO-US44039.
XX
PR 17-NOV-2000; 2000US-249468P.
XX
PA (DELTA-) DELTAGEN PROTEOMICS INC.
XX
PI Kamb CA, Richards BT, Karpilow J;
XX
DR MPI; 2002-519386/55.
XX
DR N-PSDB; ABR87379.
XX
PT Polypeptide with retinoic acid pathway activity, especially of
PT perturbagens R3, F802 and F820 for identifying a cellular target which
PT interacts with the polypeptide and for therapeutic purposes
XX
PS Claim 1; Fig 13a; 131pp; English.
XX
CC The invention relates to an isolated polypeptide (I) with retinoic acid
CC (RA) pathway activity, comprising a polypeptide sequence of Perturbagen
CC (phenotypic probe) R3, Perturbagen F802, Perturbagen F820, their
CC biologically active modifications, or biologically active fragments.
CC Also included are the polynucleotides encoding the perturbagens, a
CC vector comprising the polynucleotide, preparing an RA pathway related
CC polypeptide, a composition comprising the polypeptide, an antibody to the
CC polypeptide, screening (M) putative RA-related therapeutics, by exposing
CC a polypeptide/target interaction pair identified by a method utilising
CC the RA pathway polypeptide, to a number of agents, and recovering a
CC subpopulation of disrupting agents which competitively displace the
CC polypeptide from the target, where the disrupting agents are putative RA-
CC related therapeutics. Also include are an isolated RA pathway polypeptide
CC comprising PAT1 (a kinesin light chain-related protein) polypeptide
CC and its encoding polynucleotide, a gene therapy vector comprising the RA
CC pathway protein polypeptide or encoding or PAT1 and a host cell
CC comprising the gene therapy vector. The RA pathway polypeptide is useful
CC for identifying a cellular target that interacts with RA pathway-related
CC polypeptide, by exposing the polypeptide in vitro to putative target
CC molecules and identifying a polypeptide/target interaction pair, by
CC detecting reporter expression, where the reporter expression is
CC operatively linked to the formation of the interaction pair. (M) is a
CC yeast two-hybrid assay. The polypeptide is also useful for treating
CC an RA pathway-related condition e.g. lung cancer, Kaposi's sarcoma,
CC breast cancer, pancreatic cancer, neuroblastoma, renal cancer,
CC ovarian cancer, dermatitis, hyperkeratosis, eczema, Darier's disease,
CC Reiter's disease, psoriasis, acute promyelocytic leukaemia (APL).
XX
SQ Sequence 64 AA;
Query Match 30.88; Score 64; DB 23; Length 64;
Best Local Similarity 100.0%; Pred. No. 1.9e-54;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 61 VPKTVDNFVALATGEGKGFYKNSKFRHVITKDFMIOGSDFTRGDGTGKSTYGERFPDENF 120
DB 1 VPKTVDNFVALATGEGKGFYKNSKFRHVITKDFMIOGSDFTRGDGTGKSTYGERFPDENF 60
QY 121 KLKH 124
DB 61 KLKH 64

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RESULT 9
ID AAY92048 standard; Protein: 212 AA.
AC AAY92048;
DT 01-AUG-2000 (first entry)
DE A. niger peptidyl-prolyl cis-trans isomerase (CYPB).
KW Cyclophilin-like peptidyl prolyl cis-trans isomerase; CYPB;
KM food processing; Endoplasmic retention signal; cis-trans isomerization;
KN protein secretion; toxin; ADP-glucose pyrophosphorylase; glucanase;
KW beta-1,4-endoglucanase.
XX
XX Aspergillus niger.
XX
XX
XX Key Location/Qualifiers
XX Peptide 1..23
XX FT /label= signal_peptide
XX FT 24..212
XX FT /label= mature_protein
XX
XX WO200018934-A1.
XX
XX 06-APR-2000.
XX
XX 30-SEP-1999; 99WO-1B01669.
XX
XX 30-SEP-1998; 98GB-0021198.
XX
XX (DANI-) DANISCO AS.
XX
XX Derkx PMF, Madrid SM;
XX
XX WPI: 2000-293167/25.
XX
XX N-PSDB: AAA08772.
XX
XX New peptidyl prolyl cis-trans isomerase, designated CYPB, from
XX Aspergillus niger, useful in methods for increasing the yield of
XX secreted polypeptides, such as enzymes used in food processing, from
XX cells
XX
XX Claim 13; Page 47-48; 52pp; English.
XX
XX This sequence shows Aspergillus niger cyclophilin-like peptidyl prolyl
XX cis-trans isomerase (CYPB). CYPB is capable of catalyzing the cis-trans
XX isomerization of a peptide bond on the N-terminal side of proline
XX residues in polypeptides. CYPB are useful in methods for increasing the
XX yield of secreted polypeptides from cells. The secreted polypeptides may
XX be enzymes (such as chymosin, thrombin or alpha-galactosidase) that can
XX be used in food processing, a pest toxin, adenosine diphosphate
XX (ADP)-glucose pyrophosphorylase, a glucanase or beta-1,4-endoglucanase.
XX
XX Sequence 212 AA;
XX
XX Query Match 13.9%; Score 29; DB 21; Length 212;
XX Best Local Similarity 100.0%; Pred. No. 6.1e-20;
XX Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 85 FHRVWKDFMIOGDPTRGDTGCKSIYGE 113
DB 84 FHRVWKDFMIOGDPTRGDTGCKSIYGE 112
XX
XX RESULT 10
XX ID AAM24287 standard; Protein: 83 AA.
XX AC AAM24287;
XX

```

```

DT 12-OCT-2001 (first entry)
XX
XX Human EST encoded protein SEQ ID NO: 1812.
DE
XX
XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW diagnostics; forensic test; gene mapping; genetic disorder;
KW biodiversity; gene therapy; nutrition.
XX
XX Homo sapiens.
XX
XX WO200154477-A2.
XX
XX 02-AUG-2001.
XX
XX 25-JAN-2001; 2001WO-0S02687.
XX
XX 25-JAN-2000; 2000US-0491404.
XX
XX 17-JUL-2000; 2000US-0617746.
XX
XX 03-AUG-2000; 2000US-0631451.
XX
XX 15-SEP-2000; 2000US-0663870.
XX
XX (HSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
XX Cao Y, Drmanac RA, Zhang J, Werhman T;
XX
XX WPI: 2001-476164/51.
XX
XX N-PSDB: AAH98946.
XX
XX Isolated polypeptide for treatment of diseases, diagnostics, raising
XX antibodies and research use -
XX
XX Claim 20; Page 1183-1184; 1275pp; English.
XX
XX The present invention provides the protein and coding sequences of novel
XX proteins from a variety of organisms, including human, dog, cat, horse,
XX cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
XX urchin and tomato. These were derived from expressed sequence tags (ESTs)
XX from the organism of interest. They can be used in diagnostics,
XX forensics, gene mapping, identification of mutations, to assess
XX biodiversity and for nutritional purposes. The present sequence is a
XX protein of the invention.
XX
XX Sequence 83 AA;
XX
XX Query Match 10.6%; Score 22; DB 22; Length 83;
XX Best Local Similarity 100.0%; Pred. No. 1.7e-13;
XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 28 KKKGPKVTVKYFDLRIGDEYV 49
DB 28 KKKGPKVTVKYFDLRIGDEYV 49
XX
XX RESULT 11
XX ID ABB67378 standard; Protein: 120 AA.
XX AC ABB67378;
XX
XX 26-MAR-2002 (first entry)
XX
XX Drosophila melanogaster polypeptide SEQ ID NO 28926.
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX
XX Drosophila melanogaster.
XX
XX WO200171042-A2.
XX
XX 27-SEP-2001.
XX

```





CC proteins. The bisphosphonate binding protein, or an antibody which binds  
 CC to the binding protein can be used in the diagnosis of calcium metabolism  
 CC disorders. They can also be used to treat calcium metabolism disorders,  
 CC where the treatment is for the regulation of bone metabolism,  
 CC hypercalcaemia, bone metastases, and osteoporosis, especially by  
 CC regulation of bone metabolism via interaction with cyclosporine.

XX  
 SQ Sequence 180 AA;

Query Match 7.7%; Score 16; DB 19; Length 180;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 92 FMIOGDFTRGDGTG 107  
 |||||

Db 76 FMIOGDFTRGDGTG 91

RESULT 14

AA65277 standard; protein; 185 AA.

AC AAG65277;

DT 20-NOV-2001 (first entry)

XX Haematopoietic stem cell proliferation agent related human protein #3.

DE Haematopoietic stem cell proliferation agent; cyclophilin;

KW dyshaemopoiesis; cancer; human; mouse.

XX Homo sapiens.

PN JP2001163798-A.

PD 19-JUN-2001.

PF 03-DEC-1999; 99JP-0345542.

PR 03-DEC-1999; 99JP-0345542.

PA (KANF ) KANEKA CORP.

XX WPI; 2001-592517/67.

DT Proliferation agent for hematopoietic stem cell containing cyclophilin

PS Disclosure; Page 16-17; 19pp; Japanese.

CC The present invention provides a proliferation agent for haematopoietic  
 CC stem cells, which contains cyclophilin. This may be used in the treatment  
 CC of dyshaemopoiesis in radiotherapy and chemotherapy of various  
 CC haematopoietic organ diseases and cancers. The present sequence is a  
 CC human protein described in the exemplification of the invention.

XX  
 SQ Sequence 185 AA;

Query Match 7.7%; Score 16; DB 22; Length 185;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 83 SKFHRVIXKDFMIOGCD 98  
 |||||

Db 58 SKFHRVIXKDFMIOGCD 73

RESULT 15

AA65278

ID AAG65278 standard; protein; 185 AA.

AC AAG65278;

XX

DT 20-NOV-2001 (first entry)

XX Haematopoietic stem cell proliferation agent related murine protein #3.

DE Haematopoietic stem cell proliferation agent; cyclophilin;

KW dyshaemopoiesis; cancer; human; mouse.

XX

PN JP2001163798-A.

PD 19-JUN-2001.

PF 03-DEC-1999; 99JP-0345542.

PR 03-DEC-1999; 99JP-0345542.

PA (KANF ) KANEKA CORP.

XX WPI; 2001-592517/67.

DT Proliferation agent for hematopoietic stem cell containing cyclophilin

PS Disclosure; Page 17; 19pp; Japanese.

CC The present invention provides a proliferation agent for haematopoietic  
 CC stem cells, which contains cyclophilin. This may be used in the treatment  
 CC of dyshaemopoiesis in radiotherapy and chemotherapy of various  
 CC haematopoietic organ diseases and cancers. The present sequence is a  
 CC murine protein described in the exemplification of the invention.

XX  
 SQ Sequence 185 AA;

Query Match 7.7%; Score 16; DB 22; Length 185;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 85 FHRVIXKDFMIOGDF 100  
 |||||

Db 60 FHRVIXKDFMIOGDF 75

Search completed: April 10, 2003, 11:54:16  
 Job time : 37 secs

GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: April 10, 2003, 11:53:36 ; Search time 15 Seconds  
(Without alignments)  
407.998 Million cell updates/sec

Title: US-09-720-469a-44

Perfect score: 208  
Sequence: 1 MKVLAALALAGSVFFLLP.....VLIADCGKIEVKFAAKE 208

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues

Word size : 0

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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Issued\_Patents\_AA:\*  
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3: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
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6: /cgn2\_6/ptodata/1/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	126	60.6	126	2	US-08-482-728A-10
3	16	7.7	126	2	US-08-482-728A-11
4	16	7.7	212	1	US-08-142-897-5
5	13	6.2	205	1	US-08-142-897-6
6	12	5.8	127	2	US-08-482-728A-9
7	12	5.8	163	1	US-08-142-897-8
8	12	5.8	164	1	US-08-145-995A-9
9	12	5.8	164	2	US-08-451-747-9
10	12	5.8	164	3	US-09-134-852-9
11	12	5.8	165	1	US-08-145-995A-8
12	12	5.8	165	2	US-08-451-747-8
13	12	5.8	165	2	US-09-134-852-8
14	11	5.3	126	2	US-08-482-728A-16
15	11	5.3	134	2	US-08-482-728A-13
16	11	5.3	148	1	US-08-145-995A-6
17	11	5.3	148	1	US-08-451-747-6
18	11	5.3	148	1	US-09-134-852-6
19	11	5.3	162	1	US-08-142-897-9
20	11	5.3	162	1	US-08-145-995A-14
21	11	5.3	162	2	US-08-451-747-14
22	11	5.3	162	3	US-09-134-852-14
23	11	5.3	168	1	US-08-145-995A-12
24	11	5.3	168	1	US-08-451-747-12
25	11	5.3	168	1	US-09-134-852-12
26	11	5.3	169	1	US-08-145-995A-7
27	11	5.3	169	2	US-08-451-747-7

28	11	5.3	169	3	US-09-134-852-7	Sequence 7, Appl
29	11	5.3	175	1	US-08-145-995A-5	Sequence 5, Appl
30	11	5.3	175	2	US-08-451-747-5	Sequence 5, Appl
31	11	5.3	175	3	US-09-134-852-5	Sequence 5, Appl
32	11	5.3	273	2	US-08-989-386-8	Sequence 8, Appl
33	10	4.8	109	1	US-08-145-995A-15	Sequence 15, Appl
34	10	4.8	109	2	US-08-451-747-15	Sequence 15, Appl
35	10	4.8	109	3	US-09-134-852-15	Sequence 15, Appl
36	10	4.8	126	2	US-08-482-728A-12	Sequence 12, Appl
37	10	4.8	134	2	US-08-482-728A-14	Sequence 14, Appl
38	10	4.8	161	1	US-08-145-995A-13	Sequence 13, Appl
39	10	4.8	161	2	US-08-451-747-13	Sequence 13, Appl
40	10	4.8	161	3	US-09-134-852-13	Sequence 13, Appl
41	10	4.8	171	4	US-09-028-366-7	Sequence 7, Appl
42	10	4.8	176	1	US-08-145-995A-3	Sequence 3, Appl
43	10	4.8	176	1	US-08-145-995A-4	Sequence 4, Appl
44	10	4.8	176	2	US-08-451-747-3	Sequence 3, Appl
45	10	4.8	176	2	US-08-451-747-4	Sequence 4, Appl

## ALIGNMENTS

RESULT 1  
US-08-142-897-7  
Sequence 7, Application US/08142897  
Patent No. 5447852  
GENERAL INFORMATION:  
APPLICANT: Friedman, Jeffrey S.  
APPLICANT: Weissman, Irving L.  
TITLE OF INVENTION: No. 5447852el Cyclophilins, Associating Proteins  
TITLE OF INVENTION: and Uses  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Tracy J. Dunn  
STREET: One Market Plaza, Stewart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/142,897  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/005,917  
FILING DATE: 15-JAN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/740,375  
FILING DATE: 05-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Dunn, Tracy D.  
REGISTRATION NUMBER: 34,587  
REFERENCE/DOCKET NUMBER: 5490A-92-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 208 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-142-897-7  
Query Match 100.0%; Score 208; DB 1; Length 208;  
Best local Similarity 100.0%; Pred. No. 1,4e-188;

Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKVLLAALIGSVFELLPPGSADEKKKPKYTVKVFYFDLRIGDEVDGVRIGLFGKT 60  
DB 1 MKVLLAALIGSVFELLPPGSADEKKKPKYTVKVFYFDLRIGDEVDGVRIGLFGKT 60  
QY 61 VPKTVDFVALATGKGGKGYNSKFRHYIKDFMIOGDFTRGDTGKSIIGERPPDENE 120  
DB 61 VPKTVDFVALATGKGGKGYNSKFRHYIKDFMIOGDFTRGDTGKSIIGERPPDENE 120  
QY 121 KLKHGPGWVMANANGKPTNGSOFFITVTAMLDGKHVGVKYLEGMEVVRKVESTKT 180  
DB 121 KLKHGPGWVMANANGKPTNGSOFFITVTAMLDGKHVGVKYLEGMEVVRKVESTKT 180  
QY 181 SRDKPLKDVIIADCKIEVEKPFALAKE 208  
DB 181 SRDKPLKDVIIADCKIEVEKPFALAKE 208

## RESULT 2

US-08-482-728A-10

Sequence 10, Application US/08482728A

Patent No. 5968802

GENERAL INFORMATION:

APPLICANT: Wang, Bruce

APPLICANT: Fisher, Joseph

APPLICANT: Payan, Donald

TITLE OF INVENTION: No. 5968802el Nuclear Cyclophilin

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: Flehr, Hohbach, Test, Albritton

ADDRESSEE: &amp; Herdert

STREET: Four Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: California

COUNTRY: United States

ZIP: 94111-4187

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/482,728A

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Silva, Robin M.

REGISTRATION NUMBER: 38,304

REFERENCE/DOCKET NUMBER: A-61230/DJB/RMS

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 781-1989

TELEFAX: (415) 398-3249

TELEX: 910 277299

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 126 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-08-482-728A-10

Query Match 60.6%; Score 126; DB 2; Length 126;  
Best Local Similarity 100.0%; Pred. No. 1.9e-111;

Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 GRITELGKTVKTVDFVALATGKGGKGYNSKFRHYIKDFMIOGDFTRGDTGKSI 109  
DB 1 GRITELGKTVKTVDFVALATGKGGKGYNSKFRHYIKDFMIOGDFTRGDTGKSI 60  
QY 110 IYGERPPDENFKLKHGPGWVMANANGKPTNGSOFFITVTAMLDGKHVGVKYLEGME 169  
DB 110 IYGERPPDENFKLKHGPGWVMANANGKPTNGSOFFITVTAMLDGKHVGVKYLEGME 169

DB 61 IYGERPPDENFKLKHGPGWVMANANGKPTNGSOFFITVTAMLDGKHVGVKYLEGME 120

QY 170 VVRKVE 175  
DB 121 VVRKVE 126

## RESULT 3

US-08-482-728A-11

Sequence 11, Application US/08482728A

Patent No. 5968802

GENERAL INFORMATION:

APPLICANT: Wang, Bruce

APPLICANT: Fisher, Joseph

APPLICANT: Payan, Donald

TITLE OF INVENTION: No. 5968802el Nuclear Cyclophilin

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: Flehr, Hohbach, Test, Albritton

ADDRESSEE: &amp; Herdert

STREET: Four Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: California

COUNTRY: United States

ZIP: 94111-4187

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/482,728A

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Silva, Robin M.

REGISTRATION NUMBER: 38,304

REFERENCE/DOCKET NUMBER: A-61230/DJB/RMS

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 781-1989

TELEFAX: (415) 398-3249

TELEX: 910 277299

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 126 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-08-482-728A-11

Query Match 7.7%; Score 16; DB 2; Length 126;  
Best Local Similarity 100.0%; Pred. No. 1e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 SKFRHYIKDFMIOGSD 98  
DB 34 SKFRHYIKDFMIOGSD 49

## RESULT 4

US-08-142-897-5

Sequence 5, Application US/08142897

Patent No. 5447852

GENERAL INFORMATION:

APPLICANT: Friedman, Jeffrey S.

APPLICANT: Weissman, Irving L.

TITLE OF INVENTION: No. 5447852el Cyclophilins, Associating Proteins

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Tracy J. Dunn

STREET: One Market Plaza, Steuart Tower, Suite 2000

CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/142,897  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/005,917  
FILING DATE: 15-JAN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/740,375  
FILING DATE: 05-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Dunn, Tracy D.  
REGISTRATION NUMBER: 34,587  
REFERENCE/DOCKET NUMBER: 5490A-92-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 212 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-142-897-5

Query Match  
Best Local Similarity 7.7%; Score 16; DB 1; Length 212;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 FHRVIRKFMIGSGDFT 100  
Db 87 FHRVIRKFMIGSGDFT 102

RESULT 5  
US-08-142-897-6  
Sequence 6, Application US/08142897  
Patent No. 5447852  
GENERAL INFORMATION:  
APPLICANT: Friedman, Jeffrey S.  
APPLICANT: Weissman, Irving L.  
TITLE OF INVENTION: No. 5447852el Cyclophilins, Associating Proteins  
TITLE OF INVENTION: and Uses  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Tracy J. Dunn  
STREET: One Market Plaza, Stewart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/142,897  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/005,917  
FILING DATE: 15-JAN-1993  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/740,375  
FILING DATE: 05-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Dunn, Tracy D.  
REGISTRATION NUMBER: 34,587  
REFERENCE/DOCKET NUMBER: 5490A-92-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 205 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-142-897-6

Query Match  
Best Local Similarity 6.2%; Score 13; DB 1; Length 205;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 136 GKDTNGSOFPIIT 148  
Db 137 GKDTNGSOFPIIT 149

RESULT 6  
US-08-482-728A-9  
Sequence 9, Application US/08482728A  
Patent No. 5968802  
GENERAL INFORMATION:  
APPLICANT: Wang, Bruce  
APPLICANT: Fisher, Joseph  
APPLICANT: Payan, Donald  
TITLE OF INVENTION: No. 5968802el Nuclear Cyclophilin  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flehr, Holbach, Test, Albritton  
ADDRESSEE: & Herbert  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: United States  
ZIP: 94111-4187  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482,728A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Silva, Robin M.  
REGISTRATION NUMBER: 38,304  
REFERENCE/DOCKET NUMBER: A-61230/DJB/RMS  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 781-1989  
TELEFAX: (415) 398-3249  
TELEX: 910 277299  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 127 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-482-728A-9

Query Match  
Best Local Similarity 5.8%; Score 12; DB 2; Length 127;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 12: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 153 WLDGKHVFGKV 164  
|||||  
Db 104 WLDGKHVFGKV 115

## RESULT 7

US-08-142-897-8  
; Sequence 8, Application US/08142897  
; Patent No. 5447852  
; GENERAL INFORMATION:  
; APPLICANT: Friedman, Jeffrey S.  
; APPLICANT: Weisman, Irving L.  
; TITLE OF INVENTION: No. 5447852el Cyclophilins, Associating Proteins  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Tracy J. Dunn  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/142,897  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/005,917  
; FILING DATE: 15-JAN-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/740,375  
; FILING DATE: 05-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dunn, Tracy D.  
; REGISTRATION NUMBER: 34,587  
; REFERENCE/DOCKET NUMBER: 5490A-92-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-326-2422  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 163 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-142-897-8

Query Match 5.8%; Score 12; DB 1; Length 163;  
Best Local Similarity 100.0%; Pred. No. 0.00074;  
Matches 12: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 153 WLDGKHVFGKV 164  
|||||  
Db 120 WLDGKHVFGKV 131

RESULT 8  
US-08-145-995A-9  
; Sequence 9, Application US/08145995A  
; Patent No. 5482850  
; GENERAL INFORMATION:  
; APPLICANT: CARLOW, CLOTTIDE K.S.  
; APPLICANT: PAGE, ANTONY  
; TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC  
; TITLE OF INVENTION: COMPOUNDS

NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:

ADDRESSEE: DAVID G. CONLIN, DIKE, BRONSTEIN, ROBERTS &  
ADDRESSEE: CUSHMAN  
STREET: 130 WATER STREET  
CITY: BOSTON  
STATE: MASSACHUSETTS  
COUNTRY: USA  
ZIP: 02109

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/145,995A  
FILING DATE: 29-OCT-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: RESNICK, DAVID S.  
REGISTRATION NUMBER: 34235  
REFERENCE/DOCKET NUMBER: 43406  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 523-3400  
TELEFAX: (617) 523-6440  
TELEX: 200291 STRE UR  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 164 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-145-995A-9

Query Match 5.8%; Score 12; DB 1; Length 164;  
Best Local Similarity 100.0%; Pred. No. 0.00075;  
Matches 12: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 153 WLDGKHVFGKV 164  
|||||  
Db 121 WLDGKHVFGKV 132

RESULT 9  
US-08-451-747-9  
; Sequence 9, Application US/08451747  
; Patent No. 5821107  
; GENERAL INFORMATION:  
; APPLICANT: CARLOW, CLOTTIDE K.S.  
; APPLICANT: PAGE, ANTONY  
; TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC  
; TITLE OF INVENTION: COMPOUNDS  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: GREGORY D. WILLIAMS, NEW ENGLAND BIOLABS, INC.  
; STREET: 32 TOZER ROAD  
; CITY: BEVERLY  
; STATE: MASSACHUSETTS  
; COUNTRY: USA  
; ZIP: 01915  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/451,747  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/145,995  
; FILING DATE: 29-OCT-1993

CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: WILLIAMS, GREGORY D.  
REGISTRATION NUMBER: 30901  
REFERENCE/DOCKET NUMBER: NEB-046-DIV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (508) 927-5054  
TELEFAX: (508) 927-1705  
TELEX:  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 164 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-451-747-9

Query Match 5.8%; Score 12; DB 2; Length 164;  
Best Local Similarity 100.0%; Pred. No. 0.00075;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 153 WLDGKHVFGKV 164  
Db 121 WLDGKHVFGKV 132

RESULT 10  
US-09-134-852-9  
Sequence 9, Application US/09134852  
Patent No. 6127148  
GENERAL INFORMATION:  
APPLICANT: CARLOW, CLOTTIDE K.S.  
TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC  
NUMBER OF SEQUENCES: 21  
CURRENT APPLICATION DATA:  
CORRESPONDENCE ADDRESS:  
ADDRESSER: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &  
ATTORNEY/AGENT INFORMATION:  
NAME: RESNICK, DAVID S.  
REGISTRATION NUMBER: 34235  
REFERENCE/DOCKET NUMBER: 43406  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 523-3400  
TELEFAX: (617) 523-6440  
TELEX: 200291 STRE UR  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 164 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-09-134-852-9

Query Match 5.8%; Score 12; DB 3; Length 164;  
Best Local Similarity 100.0%; Pred. No. 0.00075;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 153 WLDGKHVFGKV 164  
Db 121 WLDGKHVFGKV 132

RESULT 11  
US-08-145-995A-8  
Sequence 8, Application US/08145995A  
Patent No. 5482850  
GENERAL INFORMATION:  
APPLICANT: CARLOW, CLOTTIDE K.S.  
TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC  
NUMBER OF SEQUENCES: 21  
CURRENT APPLICATION DATA:  
CORRESPONDENCE ADDRESS:  
ADDRESSER: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &  
ATTORNEY/AGENT INFORMATION:  
NAME: RESNICK, DAVID S.  
REGISTRATION NUMBER: 34235  
REFERENCE/DOCKET NUMBER: 43406  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 523-3400  
TELEFAX: (617) 523-6440  
TELEX: 200291 STRE UR  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 165 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-145-995A-8

Query Match 5.8%; Score 12; DB 1; Length 165;  
Best Local Similarity 100.0%; Pred. No. 0.00075;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 153 WLDGKHVFGKV 164  
Db 121 WLDGKHVFGKV 132

RESULT 12  
US-08-451-747-8  
Sequence 8, Application US/08451747  
Patent No. 5821107  
GENERAL INFORMATION:  
APPLICANT: CARLOW, CLOTTIDE K.S.  
TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC  
NUMBER OF SEQUENCES: 21

;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: GREGORY D. WILLIAMS, NEW ENGLAND BIOLABS, INC.  
;; STREET: 32 TOZER ROAD  
;; CITY: BEVERLY  
;; STATE: MASSACHUSETTS  
;; COUNTRY: USA  
;; ZIP: 01915  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patentin Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/451,747  
;; FILING DATE:  
;; CLASSIFICATION: 514  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/145,995  
;; FILING DATE: 29-OCT-1993  
;; CLASSIFICATION: 514  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: WILLIAMS, GREGORY D.  
;; REGISTRATION NUMBER: 30901  
;; REFERENCE/DOCKET NUMBER: NEB-046-DIV  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (508) 927-5054  
;; TELEFAX: (508) 927-1705  
;; TELEX:  
;; INFORMATION FOR SEQ ID NO: 8:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 165 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: unknown  
;; TOPOLOGY: unknown  
;; MOLECULE TYPE: protein  
;;  
;; US-08-451-747-8  
;;  
Query Match 5.8%, Score 12; DB 2; Length 165;  
Best Local Similarity 100.0%; Pred. No. 0.00075;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 153 WLDGKHVYFGKV 164  
Db 121 WLDGKHVYFGKV 132  
;;  
RESULT 13  
;; US-09-134-852-8  
;; Sequence 8, Application US/09134852  
;; Patent No. 6127148  
;; GENERAL INFORMATION:  
;; APPLICANT: CARLOW, CLOTHIDE K.S.  
;; TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC  
;; TITLE OF INVENTION: COMPOUNDS  
;; NUMBER OF SEQUENCES: 21  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: DAVID G. CONLIN, DIKE, BRONSTEIN, ROBERTS &  
;; ADDRESS: CUSHMAN  
;; STREET: 130 WATER STREET  
;; CITY: BOSTON  
;; STATE: MASSACHUSETTS  
;; COUNTRY: USA  
;; ZIP: 02109  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patentin Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/134,852  
;; FILING DATE:  
;; CLASSIFICATION:

;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/145,995  
;; FILING DATE: 29-OCT-1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: RESNICK, DAVID S.  
;; REGISTRATION NUMBER: 34235  
;; REFERENCE/DOCKET NUMBER: 43406  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (617) 523-3400  
;; TELEFAX: (617) 523-6440  
;; TELEX: 200291 STRE UR  
;; INFORMATION FOR SEQ ID NO: 8:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 165 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: unknown  
;; TOPOLOGY: unknown  
;; MOLECULE TYPE: protein  
;;  
;; US-09-134-852-8  
;;  
Query Match 5.8%, Score 12; DB 3; Length 165;  
Best Local Similarity 100.0%; Pred. No. 0.00075;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 153 WLDGKHVYFGKV 164  
Db 121 WLDGKHVYFGKV 132  
;;  
RESULT 14  
;; US-08-482-728A-16  
;; Sequence 16, Application US/08482728A  
;; Patent No. 5968802  
;; GENERAL INFORMATION:  
;; APPLICANT: Wang, Bruce  
;; APPLICANT: Fisher, Joseph  
;; APPLICANT: Pavan, Donald  
;; TITLE OF INVENTION: No. 5968802el Nuclear Cyclophilin  
;; NUMBER OF SEQUENCES: 21  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Flehr, Hohbach, Test, Albritton  
;; ADDRESS: & Herbert  
;; STREET: Four Embarcadero Center, Suite 3400  
;; CITY: San Francisco  
;; STATE: California  
;; COUNTRY: United States  
;; ZIP: 94111-4187  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patentin Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/482,728A  
;; FILING DATE: 07-JUN-1995  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: SILVA, RODIN M.  
;; REGISTRATION NUMBER: 38,304  
;; REFERENCE/DOCKET NUMBER: A-61230/DJB/RMS  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (415) 781-1989  
;; TELEFAX: (415) 398-3249  
;; TELEX: 910 277299  
;;  
;; INFORMATION FOR SEQ ID NO: 16:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 126 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: unknown  
;; TOPOLOGY: unknown  
;; MOLECULE TYPE: protein  
;;  
;; US-08-482-728A-16



Query Match 5.3%; Score 11; DB 2; Length 126;  
 Best Local Similarity 100.0%; Pred. No. 0.0052;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 139 TNGSOFITTV 149  
 |||||  
 Db 90 TNGSOFITTV 100

## RESULT 15

US-08-482-728A-13  
 ; Sequence 13, Application US/08482728A  
 ; Patent No. 5968802  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang, Bruce  
 ; APPLICANT: Fisher, Joseph  
 ; APPLICANT: Payan, Donald  
 ; TITLE OF INVENTION: NO. 5968802el Nuclear Cyclophilin  
 ; NUMBER OF SEQUENCES: 21  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Flehr, Hohbach, Test, Albritton  
 ; ADDRESSEE: & Herbert  
 ; STREET: Four Embarcadero Center, Suite 3400  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: United States  
 ; ZIP: 94111-4187  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentln Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/482.728A  
 ; FILING DATE: 07-JUN-1995  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Silva, Robin M.  
 ; REGISTRATION NUMBER: 38,304  
 ; REFERENCE/DOCKET NUMBER: A-61230/DJB/RMS  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 781-1989  
 ; TELEFAX: (415) 398-3249  
 ; TELEX: 910 277299  
 ; INFORMATION FOR SEQ ID NO: 13:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 134 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: unknown  
 ; TOPOLOGY: unknown  
 ; MOLECULE TYPE: protein  
 ; US-08-482-728A-13

Query Match 5.3%; Score 11; DB 2; Length 134;  
 Best Local Similarity 100.0%; Pred. No. 0.0055;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 139 TNGSOFITTV 149  
 |||||  
 Db 98 TNGSOFITTV 108

Search completed: April 10, 2003, 11:56:00  
 Job time : 16 secs





Db 181 SDDKPLKDVIIADCGKIEVEKPFATAKE 208

RESULT 2

US-09-925-301-1323

Sequence 1323, Application US/09925301

Patent No. US20020052308A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PA106

CURRENT APPLICATION NUMBER: US/09/925, 301

CURRENT FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: PCT/US00/05882

PRIOR FILING DATE: 2000-03-08

PRIOR APPLICATION NUMBER: 60/124,270

NUMBER OF SEQ ID NOS: 1694

SOFTWARE: Patentln Ver. 2.0

SEQ ID NO 1323

LENGTH: 291

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: SITE

LOCATION: (30)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE

LOCATION: (57)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-09-925-301-1323

Query Match

Best Local Similarity 100.0%; Score 208; DB 10; Length 291;

Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 84 MKVLLAALINGSVFLLLPSPADDEKKKGPVYKVFYDLRIDEDVGRVIFGLFGKT 60

Db 144 VKPTVDNFVALATGKRGKGYKSKFRHRYIKDFMIOGDFTRGDTGKSGSYGERPDENE 120

Db 144 VKPTVDNFVALATGKRGKGYKSKFRHRYIKDFMIOGDFTRGDTGKSGSYGERPDENE 203

Db 121 KKHGPGVWSMANAGKDTNCSOFFITTVKTMALDGKHVFEKVLGEMVYKVESTKTD 180

Db 204 KKHGPGVWSMANAGKDTNCSOFFITTVKTMALDGKHVFEKVLGEMVYKVESTKTD 263

Qy 181 SDDKPLKDVIIADCGKIEVEKPFATAKE 208

Db 264 SDDKPLKDVIIADCGKIEVEKPFATAKE 291

RESULT 3

US-10-043-142-11

Sequence 11, Application US/10043142

Patent No. US20020150969A1

GENERAL INFORMATION:

APPLICANT: DERRX, PATRICK M.F.

APPLICANT: MADRID, SUSAN M.

TITLE OF INVENTION: PEPTIDYL PROLYL CIS-TRANS ISOMERASES

FILE REFERENCE: 078883/0128

CURRENT APPLICATION NUMBER: US/10/043,142

CURRENT FILING DATE: 2002-01-14

PRIOR APPLICATION NUMBER: 09/806,399

PRIOR FILING DATE: 2002-03-30

PRIOR APPLICATION NUMBER: PCT/IB99/01669

PRIOR FILING DATE: 1999-09-30

PRIOR APPLICATION NUMBER: GB 9821198.0

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Patentln Ver. 2.1

SEQ ID NO 11

LENGTH: 207

TYPE: PRT

ORGANISM: Mus musculus

US-10-043-142-11

Query Match

Best Local Similarity 100.0%; Score 55; DB 12; Length 207;

Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 114 RPPDENFKLKHGPGVWSMANAGKDTNCSOFFITTVKTMALDGKHVFEKVLGEM 168

Db 113 RPPDENFKLKHGPGVWSMANAGKDTNCSOFFITTVKTMALDGKHVFEKVLGEM 167

RESULT 4

US-10-043-142-10

Sequence 10, Application US/10043142

Patent No. US20020150969A1

GENERAL INFORMATION:

APPLICANT: DERRX, PATRICK M.F.

APPLICANT: MADRID, SUSAN M.

TITLE OF INVENTION: PEPTIDYL PROLYL CIS-TRANS ISOMERASES

FILE REFERENCE: 078883/0128

CURRENT APPLICATION NUMBER: US/10/043,142

CURRENT FILING DATE: 2002-01-14

PRIOR APPLICATION NUMBER: 09/806,399

PRIOR FILING DATE: 2002-03-30

PRIOR APPLICATION NUMBER: PCT/IB99/01669

PRIOR FILING DATE: 1999-09-30

PRIOR APPLICATION NUMBER: GB 9821198.0

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Patentln Ver. 2.1

SEQ ID NO 10

LENGTH: 203

TYPE: PRT

ORGANISM: Orpiniomyces sp.

US-10-043-142-10

Query Match

Best Local Similarity 100.0%; Score 37; DB 12; Length 203;

Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 79 GYKNSKFRHRYIKDFMIOGDFTRGDTGKSGSYGERF 115

Db 73 GYKNSKFRHRYIKDFMIOGDFTRGDTGKSGSYGERF 109

RESULT 5

US-10-043-142-5

Sequence 5, Application US/10043142

Patent No. US20020150969A1

GENERAL INFORMATION:

APPLICANT: DERRX, PATRICK M.F.

APPLICANT: MADRID, SUSAN M.

TITLE OF INVENTION: PEPTIDYL PROLYL CIS-TRANS ISOMERASES

FILE REFERENCE: 078883/0128

CURRENT APPLICATION NUMBER: US/10/043,142

CURRENT FILING DATE: 2002-01-14

PRIOR APPLICATION NUMBER: 09/806,399

PRIOR FILING DATE: 2002-03-30

PRIOR APPLICATION NUMBER: PCT/IB99/01669

PRIOR FILING DATE: 1999-09-30

PRIOR APPLICATION NUMBER: GB 9821198.0

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Patentln Ver. 2.1

SEQ ID NO 5

LENGTH: 212

TYPE: PRT

ORGANISM: Aspergillus niger

US-10-043-142-5

Query Match 13.9%; Score 29; DB 12; Length 212;  
Best Local Similarity 100.0%; Pred. No. 6.8e-20;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 FHRVXKDFMIQGGDFTRGDTGKSIYGE 113  
|||||  
DB 84 FHRVXKDFMIQGGDFTRGDTGKSIYGE 112

RESULT 6  
US-09-925-300-1279  
; Sequence 1279, Application US/09925300  
; Patent No. US20020151681A1  
; GENERAL INFORMATION:  
; APPLICANT: Craig Rosen,  
; APPLICANT: Steve Ruden,  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA101  
; CURRENT APPLICATION NUMBER: US/09/925,300  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05988  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 1890  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1279  
; LENGTH: 183  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-925-300-1279

Query Match 7.2%; Score 15; DB 10; Length 183;  
Best Local Similarity 100.0%; Pred. No. 1.1e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 FHRVXKDFMIQGGDF 99  
|||||  
DB 71 FHRVXKDFMIQGGDF 85

RESULT 7  
US-09-864-761-40591  
; Sequence 40591, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharon G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; FILE REFERENCE: Aeonica-X-1  
; CURRENT APPLICATION NUMBER: US/09/864,761  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/774,203  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 49117  
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 40591  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: Homo sapiens

; FEATURE:  
; OTHER INFORMATION: MAP TO AP001538.1  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 11  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.2  
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.8  
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.6  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 15  
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.6  
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 10  
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 16  
; OTHER INFORMATION: EST\_HUMAN HIT: BF244231.1, EVALUATE 3.00e-56  
; OTHER INFORMATION: SWISSPROT HIT: P05092, EVALUATE 2.00e-49  
US-09-864-761-40591

Query Match 4.8%; Score 10; DB 10; Length 108;  
Best Local Similarity 100.0%; Pred. No. 0.039;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 GTGGKSIYGE 113  
|||||  
DB 91 GTGGKSIYGE 100

RESULT 8  
US-10-028-072-8  
; Sequence 8, Application US/10028072  
; Publication No. US20030004311A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Laureen  
; APPLICANT: Deforge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvarolt, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Geriltsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Matanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang  
; TITLE OF INVENTION:  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/028,072



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; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088741
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088810
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088858
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089599
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089907
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089947
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/090349
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090429
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090445
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090538
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
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Query Match
Best Local Similarity 100.0%; Score 10; DB 9; Length 166;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 89 IKDFMIQGD 98
Db 57 IKDFMIQGD 66
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RESULT 9
US-10-121-049-8
; Sequence 8, Application US/10121049
; Publication No. US20030022239A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C17
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US/10/121,049
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 8
; LENGTH: 166
; TYPE: PRT
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; ORGANISM: Homo Sapien
US-10-121-049-8
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Query Match
Best Local Similarity 100.0%; Score 10; DB 9; Length 166;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 89 IKDFMIQGD 98
Db 57 IKDFMIQGD 66
```

```

RESULT 10
US-10-123-904-8
; Sequence 8, Application US/10123904
; Publication No. US20030022328A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
```

```

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C54
; CURRENT APPLICATION NUMBER: US/10/123,904
; CURRENT FILING DATE: 2002-04-16
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm
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; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 8
; LENGTH: 166
; TYPE: PRT
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```

; ORGANISM: Homo Sapien
US-10-123-904-8
```

```

Query Match
Best Local Similarity 100.0%; Score 10; DB 9; Length 166;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 89 IKDFMIQGD 98
Db 57 IKDFMIQGD 66
```

```

RESULT 11
US-10-140-470-8
; Sequence 8, Application US/10140470
; Publication No. US20030022331A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
```

```
: APPLICANT: Stewart,Timothy A.
: APPLICANT: Tumas,Daniel
: APPLICANT: Watanabe,Colin K
: APPLICANT: Wood,William
: APPLICANT: Zhang,Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P330R1C160
: CURRENT APPLICATION NUMBER: US/10/140,470
: PRIOR APPLICATION removed - See Palm or File Wrapper
: NUMBER OF SEQ ID NOS: 550
: SEQ ID NO 8
: LENGTH: 166
: TYPE: PRT
: ORGANISM: Homo Saplen
US-10-140-470-8
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Query Match 4.8%; Score 10; DB 9; Length 166;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY 89 IKDFMIOGCD 98
Db 57 IKDFMIOGCD 66
```

```
RESULT 12
US-10-175-746-8
: Sequence 8, Application US/10175746
: Publication No. US20030027270A1
: GENERAL INFORMATION:
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```
: APPLICANT: Baker,Kevin P.
: APPLICANT: Beresini, Maureen
: APPLICANT: DeForge,Laura
: APPLICANT: Desnoyers,Luc
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gao,Mel-Qiang
: APPLICANT: Gerritsen,Mary E.
: APPLICANT: Goddard,Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney,Austin L.
: APPLICANT: Sherwood,Steven
: APPLICANT: Smith,Victoria
: APPLICANT: Stewart,Timothy A.
: APPLICANT: Tumas,Daniel
: APPLICANT: Watanabe,Colin K
: APPLICANT: Wood,William
: APPLICANT: Zhang,Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P330R1C353
: CURRENT APPLICATION NUMBER: US/10/175,746
: CURRENT FILING DATE: 2002-06-19
: PRIOR APPLICATION removed - See File Wrapper or Palm
: NUMBER OF SEQ ID NOS: 550
: SEQ ID NO 8
: LENGTH: 166
: TYPE: PRT
: ORGANISM: Homo Saplen
US-10-175-746-8
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Query Match 4.8%; Score 10; DB 9; Length 166;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 89 IKDFMIOGCD 98
Db 57 IKDFMIOGCD 66
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```
RESULT 13
US-10-176-918-8
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: Sequence 8, Application US/10176918
: Publication No. US20030027275A1
: GENERAL INFORMATION:
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: APPLICANT: Baker, Kevin P.
: APPLICANT: Beresini, Maureen
: APPLICANT: DeForge, Laura
: APPLICANT: Desnoyers, Luc
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gao, Mel-Qiang
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Sherwood, Steven
: APPLICANT: Smith, Victoria
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K
: APPLICANT: Wood, William
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P330R1C382
: CURRENT APPLICATION NUMBER: US/10/176,918
: CURRENT FILING DATE: 2002-06-20
: PRIOR APPLICATION removed - See File Wrapper or Palm
: NUMBER OF SEQ ID NOS: 550
: SEQ ID NO 8
: LENGTH: 166
: TYPE: PRT
: ORGANISM: Homo Saplen
US-10-176-918-8
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Query Match 4.8%; Score 10; DB 9; Length 166;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 89 IKDFMIOGCD 98
Db 57 IKDFMIOGCD 66
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RESULT 14
US-10-176-921-8
: Sequence 8, Application US/10176921
: Publication No. US20030027276A1
: GENERAL INFORMATION:
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: APPLICANT: Baker, Kevin P.
: APPLICANT: Beresini, Maureen
: APPLICANT: DeForge, Laura
: APPLICANT: Desnoyers, Luc
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gao, Mel-Qiang
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Sherwood, Steven
: APPLICANT: Smith, Victoria
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K
: APPLICANT: Wood, William
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P330R1C288
: CURRENT APPLICATION NUMBER: US/10/176,921
: CURRENT FILING DATE: 2002-06-20
: PRIOR APPLICATION removed - See File Wrapper or Palm
: NUMBER OF SEQ ID NOS: 550
: SEQ ID NO 8
: LENGTH: 166
```



Thu Apr 10 14:25:10 2003

us-09-720-469a-44.rapb

Page 7

; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-176-921-8

Query Match  
Best Local Similarity 100.0%; Score 10; DB 9; Length 166;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 89 IKDFMIQGGD 98  
|||||  
DB 57 IKDFMIQGGD 66

RESULT 15  
US-10-137-865-8  
; Sequence 8, Application US/10137865  
; Publication No. US20030032155A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3330R1C154  
; CURRENT APPLICATION NUMBER: US/10/137,865  
; CURRENT FILING DATE: 2002-05-03  
; Prior Application removed - See Palm or File Wrapper  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 8  
; LENGTH: 166  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-137-865-8

Query Match  
Best Local Similarity 100.0%; Score 10; DB 9; Length 166;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 89 IKDFMIQGGD 98  
|||||  
DB 57 IKDFMIQGGD 66

Search completed: April 10, 2003, 11:56:23  
Job time : 18 secs



GenCore version 5.1.4-p5.4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 10, 2003, 11:53:11 ; Search time 20 Seconds  
(without alignments)  
999.798 Million cell updates/sec

Title: US-09-720-469A-44

Perfect score: 208

Sequence: 1 MKVLAALAGSVFFLLP.....VIADCGKIEVFAAKE 208

Scoring table: OLIGO

Searched: 283224 seqs, 96134422 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

PIR\_73:\*  
1: pirl:\*  
2: pirl2:\*  
3: pirl3:\*  
4: pirl4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	208	100.0	208	1	CSHUB
2	98	47.1	183	2	S71547
3	98	47.1	216	2	A56861
4	55	26.4	207	2	A40516
5	23	11.1	46	2	S45724
6	19	9.1	165	2	S28020
7	17	8.2	204	2	T21587
8	16	7.7	201	2	T18573
9	16	7.7	212	2	A40047
10	16	7.7	212	2	A54204
11	15	7.2	20	2	S46488
12	15	7.2	171	2	T27371
13	15	7.2	183	2	T18578
14	14	6.7	172	2	T07950
15	14	6.7	215	2	A71261
16	13	6.2	87	2	S21218
17	13	6.2	172	2	T50769
18	13	6.2	179	2	A53522
19	13	6.2	205	2	S12324
20	13	6.2	224	2	T49204
21	13	6.2	173	1	JC5314
22	12	5.8	163	1	CSBOAB
23	12	5.8	163	1	CSPGA
24	12	5.8	164	1	CSHYAC
25	12	5.8	164	1	CSMSA
26	12	5.8	164	1	CSKTA
27	12	5.8	165	1	CSHUA
28	12	5.8	172	2	T27882
29	12	5.8	176	2	T50767

30	12	5.8	176	2	T47724	peptidyprolyl iso
31	12	5.8	179	2	S48018	peptidyprolyl iso
32	12	5.8	201	2	T50837	peptidyprolyl iso
33	12	5.8	201	2	T40819	peptidyprolyl iso
34	12	5.8	201	2	T02489	peptidyprolyl iso
35	12	5.8	204	2	T50838	peptidyprolyl iso
36	12	5.8	260	2	B53422	peptidyprolyl iso
37	12	5.8	347	2	B53522	20k cyclophilin -
38	11	5.3	162	1	CSBY	peptidyprolyl iso
39	11	5.3	162	1	CSZPA	peptidyprolyl iso
40	11	5.3	162	1	CSCK	peptidyprolyl iso
41	11	5.3	169	2	S22496	peptidyprolyl iso
42	11	5.3	173	2	T27373	peptidyprolyl iso
43	11	5.3	182	2	S30507	peptidyprolyl iso
44	11	5.3	224	2	T05766	peptidyprolyl iso
45	11	5.3	225	2	S38324	peptidyprolyl iso

#### ALIGNMENTS

##### RESULT 1

CSHUB

peptidyprolyl isomerase (EC 5.2.1.8) B precursor [validated] - human

N:Alternate names: cyclophilin B; cyclosporin A-binding protein B; S-cyclophilin

C:Species: Homo sapiens (man)

C>Date: 31-Mar-1992 #sequence,revision 31-Mar-1992 #text,change 08-Dec-2000

C:Accession: A39118; A39722; A40515; S65742

R:Price, E.R.; Zydovsky, L.D.; Jin, M.; Baker, C.H.; McKeon, F.D.; Walsh, C.T.

Proc. Natl. Acad. Sci. U.S.A. 88, 1903-1907, 1991

A:Title: Human cyclophilin B: a second cyclophilin gene encodes a peptidyprolyl iso

A:Reference number: A39118; MUID:91156714; PMID:2000394

A:Accession: A39118

A:Molecule type: mRNA

A:Residues: 1-208 <PRI>

A:Cross-references: GB:M60857; NID:g181334; PIDN:AAA52150.1; PID:g181335

R:Hassel, K.W.; Glass, J.R.; Godbout, M.; Sutcliffe, J.G.

Mol. Cell. Biol. 11, 3484-3491, 1991

A:Title: An endoplasmic reticulum-specific cyclophilin.

A:Reference number: A39722; MUID:91260697; PMID:1710767

A:Accession: A39722

A:Molecule type: mRNA

A:Residues: 1-208 <HMS>

A:Cross-references: GB:M60457; NID:g181249; PIDN:AAA35733.1; PID:g181250

R:Spik, G.; Haendler, B.; Delmas, O.; Matiller, C.; Chamoux, M.; Maes, P.; Tartar, A

J. Biol. Chem. 266, 10735-10738, 1991

A:Title: A novel secreted cyclophilin-like protein (SCYLP).

A:Reference number: A40515; MUID:91250363; PMID:2040592

A:Accession: A40515

A:Molecule type: mRNA

A:Residues: MLRLSERN',1-208 <SPI>

A:Cross-references: GB:M63573; NID:g337998; PIDN:AAA36601.1; PID:g337999

A:Note: the authors' translation begins at an ATG codon in poor context for initiation

A:Note: parts of this sequence, including the amino end of the mature form, were con

Biochim. Biophys. Acta 1293, 31-38, 1996

A:Title: Evidence that human milk isolated cyclophilin B corresponds to a truncated

A:Reference number: S65742; MUID:96186273; PMID:8652625

A:Accession: S65742

A:Molecule type: protein

A:Residues: 26-30;203 <MAR>

A:Experimental source: milk

C:Comment: This protein is distinguished from peptidyprolyl isomerase A by the pres

C:Genetics:

A:Gene: GDB:PP1B

A:Cross-references: GDB:127610; OMIM:123841

A:Map position: 15q21-15q22

C:Function:

A:Description: catalyzes the cis-trans isomerization of peptidyproline peptide bond;

C:Superfamily: peptidyprolyl isomerase; cyclophilin homology

C:Keywords: cis-trans-isomerase; cyclosporin A binding; glycoprotein; T-cell

F:1-25/Domain: signal sequence #status predicted <SIG>

F:26-203/Product: peptidylprolyl isomerase B #status experimental <MAT>  
 F:35-197/Domain: cyclophilin homology <CYP>  
 F:140/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 100.0%; Score 208; DB 1; Length 208;  
 Best Local Similarity 100.0%; Pred. No. 3e-195;  
 Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNYLAAALAGSVFELLPGSAADKKKPKVTVKVFEDLRIGDEDVGRVTFGLFGKT 60  
 DB 1 MNYLAAALAGSVFELLPGSAADKKKPKVTVKVFEDLRIGDEDVGRVTFGLFGKT 60  
 QY 61 VKRTVDNFVALATGKGFYKSKSFHRYVKDFMIOGDFTRDGTGKSIYGERPDENE 120  
 DB 61 VKRTVDNFVALATGKGFYKSKSFHRYVKDFMIOGDFTRDGTGKSIYGERPDENE 120  
 QY 121 KLRHGPVGMVSMANAGKDTNGSOFITTVKTMLDGKHVFGKYLEGMEVVRKESTKTD 180  
 DB 121 KLRHGPVGMVSMANAGKDTNGSOFITTVKTMLDGKHVFGKYLEGMEVVRKESTKTD 180  
 QY 181 SRDKPLKDVIIADCGKIEVEKPPAIKE 208  
 DB 181 SRDKPLKDVIIADCGKIEVEKPPAIKE 208

## RESULT 2

peptidylprolyl isomerase (EC 5.2.1.8) B, 20.3K - rat

N:Alternate names: cyclophilin B; PPIASE  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 15-Nov-1996 #sequence\_revision 13-Mar-1997 #text\_change 16-Jul-1999  
 C:Accession: S71547  
 R:Rucknagel, K.P.; Pfeiffer, T.; Rahfeld, J.U.; Scherfke, M.; Filscher, G.  
 submitted to the Protein Sequence Database, November 1996  
 A:Reference number: S71547  
 A:Accession: S71547  
 A:Molecule type: Protein  
 A:Residues: 1-183 <RUE>  
 A:Experimental source: liver  
 C:Superfamily: peptidylprolyl isomerase; cyclophilin homology  
 C:Keywords: cis-trans-isomerase  
 F:1-183/Product: peptidylprolyl isomerase, isoform 20.3K #status experimental <MAT>  
 F:10-172/Domain: cyclophilin homology <CYP>

Query Match 47.1%; Score 98; DB 2; Length 183;  
 Best Local Similarity 100.0%; Pred. No. 7.3e-88;  
 Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 FGLFGKTVKTYDNEFVALATGKGFYKSKSFHRYVKDFMIOGDFTRDGTGKSIYGE 113  
 DB 29 FGLFGKTVKTYDNEFVALATGKGFYKSKSFHRYVKDFMIOGDFTRDGTGKSIYGE 88  
 QY 114 RPPDENFKLKHGPGVSMANAGKDTNGSOFITTVKT 151  
 DB 89 RPPDENFKLKHGPGVSMANAGKDTNGSOFITTVKT 126

## RESULT 3

peptidylprolyl isomerase (EC 5.2.1.8) CYP-S1 precursor - mouse

N:Alternate names: cyclophilin B; cyclophilin-S1; cyclosporin A-binding protein  
 C:Species: Mus musculus (house mouse)  
 C:Date: 05-Jan-1996 #sequence\_revision 05-Jan-1996 #text\_change 16-Jul-1999  
 C:Accession: A56861; B39722; S21835  
 R:Schumacher, A.; Schroter, H.; Multhaup, G.; Nordheim, A.  
 Biochim. Biophys. Acta 1129, 13-22, 1991  
 A:Title: Murine cyclophilin-S1: a variant peptidyl-prolyl isomerase with a putative sign  
 A:Reference number: A56861; MUID:92096454; PMID:1756174  
 A:Accession: A56861  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-216 <SCH>  
 A:Experimental source: teratocarcinoma F9 cells

A:Note: sequence extracted from NCBI backbone (NCBIN:73234; NCBI:73239)  
 A:Note: parts of this sequence, including the amino end of the mature protein, were c

R:Haas, K.W.; Glass, J.R.; Godbout, M.; Sutcliffe, J.G.  
 Mol. Cell. Biol. 11, 3484-3491, 1991  
 A:Title: An endoplasmic reticulum-specific cyclophilin.  
 A:Reference number: A39722; MUID:91260697; PMID:1710767  
 A:Accession: B39722  
 A:Molecule type: mRNA

A:Residues: 9-216 <HAS>  
 A:Cross-references: GB:M60456; NID:9192864; PIDN:AAA37498.1; PID:9192865  
 R:Nordheim, A.  
 submitted to the EMBL Data Library, May 1991  
 A:Reference number: S21835  
 A:Accession: S21835

A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 9-216 <NOR>  
 A:Cross-references: EMBL:X58990; NID:953034; PIDN:CAA41736.1; PID:953035  
 C:Comment: This protein is distinguished from peptidylprolyl isomerase A by the prese  
 C:Superfamily: peptidylprolyl isomerase; cyclophilin homology  
 C:Keywords: cis-trans-isomerase; cyclosporin A binding; endoplasmic reticulum; T-cell  
 F:1-33/Domain: signal sequence #status predicted <SIG>  
 F:34-216/Product: peptidylprolyl isomerase B #status predicted <MAT>  
 F:43-205/Domain: cyclophilin homology <CYP>

Query Match 47.1%; Score 98; DB 2; Length 216;  
 Best Local Similarity 100.0%; Pred. No. 8.3e-88;  
 Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 FGLFGKTVKTYDNEFVALATGKGFYKSKSFHRYVKDFMIOGDFTRDGTGKSIYGE 113  
 DB 62 FGLFGKTVKTYDNEFVALATGKGFYKSKSFHRYVKDFMIOGDFTRDGTGKSIYGE 121  
 QY 114 RPPDENFKLKHGPGVSMANAGKDTNGSOFITTVKT 151  
 DB 122 RPPDENFKLKHGPGVSMANAGKDTNGSOFITTVKT 159

## RESULT 4

peptidylprolyl isomerase (EC 5.2.1.8) (S-cyclophilin) precursor - chicken

C:Species: Gallus gallus (chicken)  
 C:Date: 28-Feb-1992 #sequence\_revision 28-Feb-1992 #text\_change 16-Jul-1999  
 C:Accession: A40516  
 R:Caroni, P.; Rothenfluh, A.; McGlynn, E.; Schneider, C.  
 J. Biol. Chem. 266, 10739-10742, 1991  
 A:Title: S-cyclophilin. New member of the cyclophilin family associated with the secr  
 A:Reference number: A40516; MUID:91250364; PMID:2040593  
 A:Accession: A40516  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-207 <CAR>  
 A:Cross-references: GB:M63553; NID:9212648; PIDN:AAA49064.1; PID:9212649  
 C:Superfamily: peptidylprolyl isomerase; cyclophilin homology  
 C:Keywords: cis-trans-isomerase; cyclosporin A binding  
 F:34-196/Domain: cyclophilin homology <CYP>

Query Match 26.4%; Score 55; DB 2; Length 207;  
 Best Local Similarity 100.0%; Pred. No. 7.9e-46;  
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 114 RPPDENFKLKHGPGVSMANAGKDTNGSOFITTVKTMLDGKHVFGKYLEG 168  
 DB 113 RPPDENFKLKHGPGVSMANAGKDTNGSOFITTVKTMLDGKHVFGKYLEG 167

## RESULT 5

peptidylprolyl isomerase (EC 5.2.1.8) B - bovine (fragment)

N:Alternate names: cyclophilin B  
 C:Species: Bos primigenius taurus (cattle)  
 C:Date: 25-Dec-1994 #sequence\_revision 14-Jul-1995 #text\_change 11-Jun-1999  
 C:Accession: S45724

R:Galat, A.; Bouet, F.  
FEBS Lett. 347, 31-36, 1994  
A:Title: Cyclophilin-B is an abundant protein whose conformation is similar to cyclophilin  
A:Reference number: S45724; MUID:94283623; PMID:8013656  
A:Accession: S45724

A:Molecule type: protein  
A:Residues: 1-46 <GAL>

C:Superfamily: peptidylprolyl isomerase; cyclophilin homology  
C:Keywords: cis-trans-isomerase; cyclosporin A binding

Query Match 11.1%; Score 23; DB 2; Length 46;  
Best Local Similarity 100.0%; Pred. No. 4.2e-15;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 DEKKGPKVTYKYPFLRIGDED 48  
|||||  
DB 1 DEKKGPKVTYKYPFLRIGDED 23

RESULT 6  
S28020

peptidylprolyl isomerase (EC 5.2.1.8) - Streptomyces chrysomallus  
N:Alternate names: cyclophilin A; cyclosporin A-binding protein  
C:Species: Streptomyces chrysomallus

C>Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 16-Jul-1999

C:Accession: S28020; S25676  
R:Paul, A.; Uehlein, M.; Bang, H.; Schlumbohm, W.; Keller, U.

Mol. Microbiol. 6, 3551-3558, 1992

A:Title: Streptomyces possess peptidyl-prolyl cis-trans isomerases that strongly resemble  
A:Reference number: S28020; MUID:93116593; PMID:1474897

A:Accession: S28020

A:Molecule type: DNA

A:Residues: 1-165 <PAB>

A:Cross-references: EMBL:J15137; NID:g46835; PIDN:CAA78840.1; PID:g46836  
C:Superfamily: peptidylprolyl isomerase; cyclophilin homology

C:Keywords: cis-trans-isomerase; cyclosporin A binding

F:2-165/Domain: cyclophilin homology <CYP>

Query Match 9.1%; Score 19; DB 2; Length 165;  
Best Local Similarity 100.0%; Pred. No. 9.5e-11;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 QGGDFTRGDTGKSTYGE 113  
|||||  
DB 62 QGGDFTRGDTGKSTYGE 80

RESULT 7  
T21587

peptidylprolyl isomerase (EC 5.2.1.8) F31C3.1 [similarity] - Caenorhabditis elegans  
N:Contains: cyclophilin  
C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 02-Sep-2000

C:Accession: T21587

R:Cottage, A.  
submitted to the EMBL Data Library, March 1997

A:Reference number: Z19446

A:Accession: T21587

A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA

A:Residues: 1-204 <WIL>

A:Cross-references: EMBL:Z92784; PIDN:CAB07192.1; GSPDB:GN00019; CESP:F31C3.1  
A:Experimental source: clone F31C3

C:Genetics:

A:Gene: CESP:F31C3.1

A:Map position: 1

A:Insertions: 69/3  
C:Superfamily: peptidylprolyl isomerase; cyclophilin homology

C:Keywords: cis-trans-isomerase

F:28-190/Domain: cyclophilin homology <CYP>

Query Match 8.2%; Score 17; DB 2; Length 204;  
Best Local Similarity 100.0%; Pred. No. 1e-08;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 91 DFMIQGDFTFRGDTGG 107  
|||||  
DB 84 DFMIQGDFTFRGDTGG 100

RESULT 8  
T18573

peptidylprolyl isomerase (EC 5.2.1.8) precursor - Caenorhabditis elegans

N:Alternate names: cyclophilin

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 02-Sep-2000

C:Accession: T18573; T16351

R:Page, A.P.  
submitted to the EMBL Data Library, May 1995

A:Reference number: Z18981

A:Accession: T18573  
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-201 <PAG>  
A:Cross-references: EMBL:U27354; PIDN:AA47124.1; GSPDB:GN00021; CESP:cyp-6

A:Experimental source: strain N2

R:Paich, A.  
submitted to the EMBL Data Library, March 1996

A:Description: The sequence of C. elegans cosmid F4269.

A:Reference number: Z18498

A:Accession: T16351

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-201 <PAI>  
A:Cross-references: EMBL:U00051; NID:g1216305; PID:g485120; PIDN:AAA91355.1; CESP:F42

A:Experimental source: strain Bristol N2

C:Genetics:

A:Gene: CESP:cyp-6  
A:Map position: 3

A:Insertions: 66/3

C:Superfamily: peptidylprolyl isomerase; cyclophilin homology

C:Keywords: cis-trans-isomerase

F:25-187/Domain: cyclophilin homology <CYP>

Query Match 7.7%; Score 16; DB 2; Length 201;  
Best Local Similarity 100.0%; Pred. No. 9.5e-08;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 FMIOGDFTRGDTGG 107  
|||||  
DB 82 FMIOGDFTRGDTGG 97

RESULT 9  
A40047  
peptidylprolyl isomerase (EC 5.2.1.8) (cyclophilin C) - mouse

C:Species: Mus musculus (house mouse)

C>Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 16-Jul-1999

C:Accession: A40047

R:Friedman, J.; Weisman, I.  
Cell 66, 799-806, 1991

A:Title: Two cytoplasmic candidates for immunophilin action are revealed by affinity

A:Reference number: A40047; MUID:91347379; PMID:1652374

A:Accession: A40047

A:Molecule type: DNA  
A:Residues: 1-212 <FRI>

A:Cross-references: GB:M74227; NID:g192898; PIDN:AAA37511.1; PID:g192899

C:Comment: This protein binds the immunosuppressive drug cyclosporin A.  
C:Superfamily: peptidylprolyl isomerase; cyclophilin homology

C:Keywords: cis-trans-isomerase; cyclosporin A binding

F:37-199/Domain: cyclophilin homology <CYP>

Query Match 7.7%; Score 16; DB 2; Length 212;  
Best Local Similarity 100.0%; Pred. No. 9.9e-08;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 85 FHRVTKDFMIOGDF 100  
 Db 87 FHRVTKDFMIOGDF 102

## RESULT 10

peptidylprolyl isomerase (EC 5.2.1.8) C precursor - human  
 N:Alternate names: cyclophilin C  
 C:Species: Homo sapiens (man)  
 C>Date: 22-Oct-1994 #sequence\_revision 18-Nov-1994 #text\_change 16-Jul-1999  
 A:Accession: A54204  
 R:Schmeider, H.; Charara, N.; Schmitz, R.; Wehrli, S.; Mikol, V.; Zurini, M.G.; Quesniau  
 Biochemistry 33, 8218-8224, 1994  
 A:Title: Human cyclophilin C: primary structure, tissue distribution, and determination  
 A:Reference number: A54204; MUID:94304830; PMID:8031755  
 A:Accession: A54204  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-212 <SCH>  
 A:Cross-references: GB:S71018; NID:9547303; PIDN:AAB31350.1; PID:9547304  
 A:Experimental source: kidney  
 A>Note: Sequence extracted from NCBI backbone (NCBIN:149387, NCBI:P:149388)  
 C:Genetics:  
 A:Gene: GDB:PPIC  
 A:Cross-references: GDB:136196; OMIM:123842  
 A:Map position: 15q21-15q22  
 C:Superfamily: peptidylprolyl isomerase; cyclophilin homology  
 C:Keywords: cis-trans-isomerase; cyclosporin A binding  
 F:37-199/Domain: cyclophilin homology <CYP>

## Query Match

Best Local Similarity 7.2%; Score 16; DB 2; Length 212;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 83 SKFHRVTKDFMIOGCD 98  
 Db 85 SKFHRVTKDFMIOGCD 100

## RESULT 11

peptidylprolyl isomerase (EC 5.2.1.8) - bovine (fragment)  
 N:Alternate names: peptidylprolyl cis-trans-isomerase  
 N:Contains: cyclophilin  
 C:Species: Bos primigenius taurus (cattle)  
 C>Date: 15-Jul-1995 #sequence\_revision 26-Jul-1996 #text\_change 02-Sep-2000  
 A:Accession: S46488  
 R:Bose, S.; Muecke, M.; Freedman, R.B.  
 Biochem. J. 300, 871-875, 1994  
 A:Title: The characterization of a cyclophilin-type peptidyl prolyl cis-trans-isomerase  
 A:Reference number: S46488; MUID:94280416; PMID:8010972  
 A:Accession: S46488  
 A:Molecule type: protein  
 A:Residues: 1-20 <BOS>  
 C:Superfamily: peptidylprolyl isomerase; cyclophilin homology  
 C:Keywords: cis-trans-isomerase; cyclosporin A binding

## Query Match

Best Local Similarity 7.2%; Score 15; DB 2; Length 20;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 31 GPKVTVKVFDFLRIG 45  
 Db 6 GPKVTVKVFDFLRIG 20

## RESULT 12

peptidylprolyl isomerase (EC 5.2.1.8) Y75B12B.2 [similarity] - Caenorhabditis elegans  
 N:Contains: cyclophilin  
 C:Species: Caenorhabditis elegans  
 C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 02-Sep-2000

C:Accession: T27371  
 R:White, S.  
 Submitted to the EMBL Data Library, October 1998  
 A:Reference number: T27371  
 A:Accession: T27371  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-171 <WIL>  
 A:Cross-references: EMBL:AL032663; PIDN:CAA21760.1; GSPDB:GN00023; CESP:Y75B12B.2  
 A:Experimental source: clone Y75B12B  
 C:Genetics:  
 A:Gene: CESP:Y75B12B.2  
 A:Map position: 5  
 A:Introns: 23/3; 107/3  
 C:Superfamily: peptidylprolyl isomerase; cyclophilin homology  
 C:Keywords: cis-trans-isomerase  
 F:3-171/Domain: cyclophilin homology <CYP>

## Query Match

Best Local Similarity 7.2%; Score 15; DB 2; Length 171;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 148 TVKTAWLDGKHVFG 162  
 Db 123 TVKTAWLDGKHVFG 137

## RESULT 13

peptidylprolyl isomerase (EC 5.2.1.8) cyp-11 [similarity] - Caenorhabditis elegans  
 N:Contains: cyclophilin  
 C:Species: Caenorhabditis elegans  
 C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 08-Sep-2000  
 A:Accession: T18578; T24269  
 R:Page, A.P.; MacNiven, K.  
 Submitted to the EMBL Data Library, August 1995  
 A:Reference number: T18578  
 A:Accession: T18578  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-183 <PAG>  
 A:Cross-references: EMBL:U34955; PIDN:AAC47115.1  
 A:Experimental source: strain Bristol N2  
 R:Slins, M.  
 Submitted to the EMBL Data Library, October 1995  
 A:Reference number: T19867  
 A:Accession: T24269  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-183 <WIL>  
 A:Cross-references: EMBL:Z66499; PIDN:CAA91297.1; GSPDB:GN00020; CESP:T01B7.4  
 A:Experimental source: clone T01B7  
 C:Genetics:  
 A:Gene: CESP:cyp-11  
 A:Map position: 2  
 A:Introns: 34/3; 87/3; 148/1  
 C:Superfamily: peptidylprolyl isomerase; cyclophilin homology  
 C:Keywords: cis-trans-isomerase  
 F:16-183/Domain: cyclophilin homology <CYP>

## Query Match

Best Local Similarity 7.2%; Score 15; DB 2; Length 183;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 85 FHRVTKDFMIOGDF 99  
 Db 71 FHRVTKDFMIOGDF 85

## RESULT 14

peptidylprolyl isomerase (EC 5.2.1.8) 1 - Chlamydomonas reinhardtii  
 N:Alternate names: cyclophilin 1; peptidyl-prolyl cis-trans isomerase

C:/Species: Chlamydomonas reinhardtii  
 C:/Date: 21-May-1999 #sequence\_revision 21-May-1999 #text\_change 08-Oct-1999  
 C:/Accession: T07950  
 R:/Somanchi, A.; Handley, E.R.; Moroney, J.V.  
 Submitted to the EMBL Data Library, March 1998  
 A:/Description: Identification of a cyclophilin cDNA from Chlamydomonas reinhardtii.  
 A:/Reference number: 216241  
 A:/Accession: T07950  
 A:/Status: preliminary; translated from GB/EMBL/DBJ  
 A:/Molecule type: mRNA  
 A:/Residues: 1-172 <SOM>  
 A:/Cross-references: EMBL:AF052206; NID:g2959711; PIDN:AAC05639.1; PID:g2959712  
 C:/Genetics:  
 A:/Gene: cyp1  
 C:/Superfamily: peptidylprolyl isomerase; cyclophilin homology  
 C:/Keywords: cis-trans-isomerase; cyclosporin A binding  
 F:/3-171/Domain: cyclophilin homology <CYP>

## Query Match

6.7%; Score 14; DB 2; Length 172;  
 Best Local Similarity 100.0%; Pred. No. 7.5e-06;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 151 TAWLDGKHVYFGKV 164

|||||

DB 126 TAWLDGKHVYFGKV 139

## RESULT 15

A71261  
 peptidylprolyl isomerase (EC 5.2.1.8) TP0947 [similarity] - syphilis spirochete

N:/Contains: cyclophilin

C:/Species: Treponema pallidum subsp. pallidum (syphilis spirochete)

C:/Date: 24-Jul-1998 #sequence\_revision 24-Jul-1998 #text\_change 08-Sep-2000

C:/Accession: A71261

R:/Fraser, C.M.; Morris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin

trson, J.; Khatala, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; MCD

Science 281, 375-388, 1998

A:/Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.

A:/Reference number: A71250; MUID:98332770; PMID:9665876

A:/Accession: A71261

A:/Status: preliminary; nucleic acid sequence not shown; translation not shown

A:/Molecule type: DNA

A:/Residues: 1-215 <COL>

A:/Cross-references: GB:AE001263; GB:AE000520; NID:g3323266; PIDN:AAC65904.1; PID:g332326

A:/Experimental source: strain Nichols

C:/Genetics:

C:/Superfamily: peptidylprolyl isomerase; cyclophilin homology

C:/Keywords: cis-trans-isomerase

F:/34-206/Domain: cyclophilin homology <CYP>

## Query Match

6.7%; Score 14; DB 2; Length 215;  
 Best Local Similarity 100.0%; Pred. No. 9e-06;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 FHRVINDFMIOGSD 98

|||||

DB 89 FHRVINDFMIOGSD 102

Search completed: April 10, 2003, 11:55:39  
 Job time : 21 secs





GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: April 10, 2003, 11:52:26 ; Search time 12 Seconds

(without alignments)  
718.923 Million cell updates/sec

Title: US-09-720-469A-44

Perfect score: 208  
Sequence: 1 MKVLAALALGSAVFLLLP.....VILADCGKIEVEKFAIAKE 208

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size: 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	208	100.0	208	1	CYPR_HUMAN
2	98	47.1	208	1	CYPR_MOUSE
3	77	37.0	208	1	CYPR_BOVIN
4	63	30.3	208	1	CYPR_RAT
5	55	26.4	207	1	CYPR_CHICK
6	19	9.1	165	1	PII_STRICH
7	17	8.2	204	1	CYPS_CABEL
8	16	7.7	201	1	CYPS_CABEL
9	16	7.7	212	1	CYPC_HUMAN
10	16	7.7	212	1	CYPC_MOUSE
11	15	7.2	171	1	CYPR_CABEL
12	15	7.2	183	1	CYPR_CABEL
13	14	6.7	215	1	PIIB_TREPA
14	13	6.2	150	1	CYPR_ALICE
15	13	6.2	205	1	CYPR_YEAST
16	13	5.8	163	1	CYPR_BOVIN
17	12	5.8	163	1	CYPR_CRILLO
18	12	5.8	163	1	CYPR_MOUSE
19	12	5.8	163	1	CYPR_RAT
20	12	5.8	163	1	CYPR_URIFA
21	12	5.8	164	1	CYPR_HUMAN
22	12	5.8	171	1	CYPR_CABEL
23	12	5.8	172	1	CYPR_LUPULU
24	12	5.8	260	1	CYPR_ARATH
25	11	5.3	161	1	CYPR_YEAST
26	11	5.3	162	1	CYPR_CANAL
27	11	5.3	162	1	CYPR_SCHPO
28	11	5.3	169	1	CYPR_ARATH
29	11	5.3	173	1	CYPR_CABEL
30	11	5.3	182	1	CYPR_YEAST
31	11	5.3	225	1	CYPR_YEAST
32	11	5.3	225	1	CYPR_YEAST
33	11	5.3	370	1	CYPR_BOVIN
					CYPR_HUMAN

## ALIGNMENTS

RESULT 1	CYPR_HUMAN	STANDARD:	PRG:	208 AA.
AC	P23284;			
DT	01-NOV-1991 (Rel. 20, Created)			
DT	01-NOV-1991 (Rel. 20, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Peptidyl-prolyl cis-trans isomerase B precursor (EC 5.2.1.8) (PPIase)			
DE	(Rotamase) (Cyclophilin B) (S-cyclophilin) (SCYLP) (CYP-S1).			
GN	PIIB OR CYPR.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_Taxid=9606;			
RN	[1]			
RX	SEQUENCE FROM N.A., AND SEQUENCE OF 26-40.			
RX	MEDLINE-91156714; PubMed-2000394;			
RA	Price E.R., Zydzowsky L.D., Jin M., Hunter C.H., McKeon F.D.,			
RA	Walsh C.T.;			
RT	"Human cyclophilin B: a second cyclophilin gene encodes a peptidyl-			
RT	prolyl isomerase with a signal sequence."			
RL	Proc. Natl. Acad. Sci. U.S.A. 88:1903-1907(1991).			
RN	[2]			
RX	SEQUENCE FROM N.A.			
RX	MEDLINE-91250363; PubMed-2040592;			
RA	Spik G., Heendler B., Delmas O., Mariller C., Chamoux M., Maes P.,			
RA	Tartar A., Montreuil J., Stedman K., Kocher H.P., Keller R.,			
RA	Hestrand P.C., Moyva N.R.;			
RA	"A novel secreted cyclophilin-like protein (SCYLP)."			
RL	J. Biol. Chem. 266:10735-10738(1991).			
RN	[3]			
RX	SEQUENCE OF 2-208 FROM N.A.			
RX	MEDLINE-91260697; PubMed-1710767;			
RA	Hassel K.W., Glass J.R., Godbout M., Sutcliffe J.G.;			
RA	"An endoplasmic reticulum-specific cyclophilin.";			
RL	Mol. Cell. Biol. 11:3484-3491(1991).			
RN	[4]			
RX	SEQUENCE OF 64-76 AND 151-157.			
RX	MEDLINE-93162043; PubMed-1286667;			
RA	Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,			
RA	Vandekerckhove J.;			
RT	"Microsequences of -145 proteins recorded in the two-dimensional gel			
RT	protein database of normal human epidermal keratinocytes.";			
RL	Electrophoresis 13:960-969(1992).			
RN	[5]			
RP	SUBCELLULAR LOCATION.			
RP	MEDLINE-92112948; PubMed-1530944;			
RA	Arber S., Krause K.-H., Caroni P.;			
RT	"S-cyclophilin is retained intracellularly via a unique COOH-terminal			
RT	sequence and colocalizes with the calcium storage protein			
RT	calreticulin.";			
RL	J. Cell Biol. 116:113-125(1992).			
RN	[6]			
RX	X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS).			
RX	MEDLINE-94255495; PubMed-8197205;			
RA	Mikol V., Kallen J., Walkinshaw M.D.;			

34	10	4.8	161	1	CYPR_ECHGR	P14088 echinococcu
35	10	4.8	164	1	CYPR_BLAGR	P54985 blattella g
36	10	4.8	164	1	CYPR_HEMPU	P91791 hemipterote
37	10	4.8	166	1	CYPR_HUMAN	O9Y3C6 homo sapien
38	10	4.8	166	1	CYPR_MOUSE	O9D0K5 mus musculu
39	10	4.8	171	1	CYPR_BRANA	P24525 brassica ra
40	10	4.8	172	1	CYPR_ARATH	P34790 arabidopsis
41	10	4.8	172	1	CYPR_CATRO	O39613 catharanthu
42	10	4.8	192	1	CYPR_MAIZE	P21569 zea mays (m
43	10	4.8	206	1	CYPR_CABEL	P52009 caenorhabdi
44	10	4.8	206	1	CYPR_MOUSE	O99K77 mus musculu
45	10	4.8	206	1	CYPR_RAT	P29117 rattus norv

```

RT      *X-ray structure of a cyclophilin B/cyclosporin complex: comparison
RT      with cyclophilin A and delineation of its calcineurin-binding
RT      domain."
RT      Proc. Natl. Acad. Sci. U.S.A. 91:5183-5186(1994).
CC      -1- FUNCTION: PPIases accelerate the folding of proteins. It catalyzes
CC      the cis-trans isomerization of proline imidic peptide bonds in
CC      oligopeptides.
CC      -1- CATALYTIC ACTIVITY: Peptidylproline (omega-180) = peptidylproline
CC      (omega-0).
CC      -1- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.
CC      -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC      -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
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CC      or send an email to license@isb-sib.ch).
CC      -----
CC      DR      EMBL: M60857; AAA52150.1; -.
CC      DR      EMBL: M63573; AAA36501.1; ALT_INIT.
CC      DR      EMBL: M60457; AAA35733.1; -.
CC      DR      PIR: A39118; CSHDB.
CC      DR      PIR: A40515; A40515.
CC      DR      PDB: 1CYN; 29-JAN-96.
CC      DR      SWISS-2DPAGE: P23284; HUMAN.
CC      DR      Aarhus/Chent-2DPAGE; 117; NEPHGE.
CC      DR      Genev: HGNC:9255; PPIB.
CC      DR      MIM: 123841; -.
CC      DR      InterPro: IPR002130; CSA_PPIase.
CC      DR      Pfam: PF00160; pro_Isoomerase; 1.
CC      DR      PRINTS: PR00153; CSAPPISMRASE.
CC      DR      PROSITE: PS00170; CSA_PPIASE_1; 1.
CC      DR      PROSITE: PS50072; CSA_PPIASE_2; 1.
CC      DR      Cyclosporin: Isoomerase; Rotamase; Signal; Endoplasmic reticulum;
CC      KW      Multigene family; 3D-structure.
CC      FT      SIGNAL 1 25
CC      FT      CHAIN 26 208 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B.
CC      FT      SITE 199 208 PREVENT SECRETION FROM ER.
CC      SQ      SEQUENCE 208 AA; 22742 MW; A814481B7EBD4579 CRC64;

Query Match 100.0%; Score 208; DB 1; Length 208;
Best Local Similarity 100.0%; Pred. No. 8,5e-184; Indels 0; Gaps 0;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MKVLLAALAGSVFFLLPGPSAADEKKKGPVTYVYFDLRIIGDEDVGRVIFGLFGKT 60
QY      1 MKVLLAALAGSVFFLLPGPSAADEKKKGPVTYVYFDLRIIGDEDVGRVIFGLFGKT 60
DB      1 MKVLLAALAGSVFFLLPGPSAADEKKKGPVTYVYFDLRIIGDEDVGRVIFGLFGKT 60
QY      61 VPKTVDNFVALATGEGKFGYKNSKFRVYIDFMIOGDDFRGGTGGKSTYGERFPDENF 120
QY      61 VPKTVDNFVALATGEGKFGYKNSKFRVYIDFMIOGDDFRGGTGGKSTYGERFPDENF 120
DB      61 VPKTVDNFVALATGEGKFGYKNSKFRVYIDFMIOGDDFRGGTGGKSTYGERFPDENF 120
QY      121 KLRHYGQWYMANAGKDTNGSOFFITTVKTAMLDGKHVYFGVGLGMEYVRYKVESTKTD 180
QY      121 KLRHYGQWYMANAGKDTNGSOFFITTVKTAMLDGKHVYFGVGLGMEYVRYKVESTKTD 180
DB      121 KLRHYGQWYMANAGKDTNGSOFFITTVKTAMLDGKHVYFGVGLGMEYVRYKVESTKTD 180
QY      181 SRDKPLADVIADCGKIEVERPAIAKE 208
QY      181 SRDKPLADVIADCGKIEVERPAIAKE 208
DB      181 SRDKPLADVIADCGKIEVERPAIAKE 208

RESULT 2
CYPB_MOUSE
ID      CYPB_MOUSE STANDARD: PRT; 208 AA.
AC      P24369;
DT      01-MAR-1992 (Rel. 21, Created)
DT      01-MAR-1992 (Rel. 21, Last sequence update)
DT      15-JUN-2002 (Rel. 41, Last annotation update)
DE      Peptidyl-prolyl cis-trans isomerase B precursor (EC 5.2.1.8) (PPIase)
DE      (Notamase) (Cyclophilin B) (S-cyclophilin) (SCYLP) (CYP-S1).

```

```

CN      PPIB.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=91260697; PubMed=1710767;
RA      Hasel K.W., Glass J.R., Godbout M., Sutcliffe J.C.;
RT      "An endoplasmic reticulum-specific cyclophilin.";
RL      Mol. Cell. Biol. 11:3484-3491(1991).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      STRAIN=C57BL/6; PubMed=1756174;
RA      Schumacher A., Schroeter H., Multhaup G., Nordheim A.;
RT      "Murine cyclophilin-S1: a variant peptidyl-prolyl isomerase with a
RT      putative signal sequence expressed in differentiating f9 cells.";
RL      Biochim. Biophys. Acta 1129:13-22(1991).
CC      -1- FUNCTION: PPIases accelerate the folding of proteins. It catalyzes
CC      the cis-trans isomerization of proline imidic peptide bonds in
CC      oligopeptides.
CC      -1- CATALYTIC ACTIVITY: Peptidylproline (omega-180) = peptidylproline
CC      (omega-0).
CC      -1- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.
CC      -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (by similarity).
CC      -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC      entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
CC      DR      EMBL: M60456; AAA37498.1; -.
CC      DR      EMBL: X58990; CAA41736.1; -.
CC      DR      PIR: B39722; B39722.
CC      DR      PIR: S21835; S21835.
CC      DR      HSSP: P23284; 1CYN.
CC      DR      MGD: MGI:97750; PPIB.
CC      DR      InterPro: IPR002130; CSA_PPIase.
CC      DR      Pfam: PF00160; pro_Isoomerase; 1.
CC      DR      PRINTS: PR00153; CSAPPISMRASE.
CC      DR      PROSITE: PS00170; CSA_PPIASE_1; 1.
CC      DR      PROSITE: PS50072; CSA_PPIASE_2; 1.
CC      DR      Cyclosporin: Isoomerase; Rotamase; Signal; Endoplasmic reticulum;
CC      KW      Multigene family.
CC      FT      SIGNAL 1 25 BY SIMILARITY.
CC      FT      CHAIN 26 208 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B.
CC      FT      SITE 199 208 PREVENT SECRETION FROM ER
CC      FT      (BY SIMILARITY).
CC      SQ      SEQUENCE 208 AA; 22713 MW; 4B8DF5AE40BA3A7 CRC64;

Query Match 47.1%; Score 98; DB 1; Length 208;
Best Local Similarity 100.0%; Pred. No. 9,8e-83; Indels 0; Gaps 0;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      54 FGLFGTVPKTVDNFVALATGEGKFGYKNSKFRVYIDFMIOGDDFRGGTGGKSTYGE 113
QY      54 FGLFGTVPKTVDNFVALATGEGKFGYKNSKFRVYIDFMIOGDDFRGGTGGKSTYGE 113
DB      54 FGLFGTVPKTVDNFVALATGEGKFGYKNSKFRVYIDFMIOGDDFRGGTGGKSTYGE 113
QY      114 RPPDENFKLRHYGQWYMANAGKDTNGSOFFITTVKT 151
QY      114 RPPDENFKLRHYGQWYMANAGKDTNGSOFFITTVKT 151
DB      114 RPPDENFKLRHYGQWYMANAGKDTNGSOFFITTVKT 151

RESULT 3
CYPB_BOVIN
ID      CYPB_BOVIN STANDARD: PRT; 208 AA.
AC      P80311;
DT      01-JUN-1994 (Rel. 29, Created)

```

DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Peptidyl-prolyl cis-trans isomerase B precursor (EC 5.2.1.8) (PPIase)  
 DE (Rotamase) (Cyclophilin B) (S-cyclophilin) (SCYLP).  
 GN PPIB.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 CC NCBI\_Taxid=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=uterus;  
 RA Carrello A., Mark P.J., House A.K., Ratajczak T.;  
 RL Submitted (JAN-1993) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE OF 26-71.  
 RC TISSUE=Brain;  
 RX MEDLINE=94283623; PubMed=8013656;  
 RA Galat A., Bouet F.;  
 RT "Cyclophilin-B is an abundant protein whose conformation is similar  
 to cyclophilin-A.";  
 RL FEBS Lett. 347:31-36(1994).  
 RN [3]  
 RP SEQUENCE OF 26-45.  
 RX MEDLINE=94280416; PubMed=8010972;  
 RA Bose S., Muecke M., Freedman R.B.;  
 RT "The characterization of a cyclophilin-type peptidyl prolyl  
 cis-trans-isomerase from the endoplasmic reticulum lumen.";  
 RL Biochem. J. 300:871-875(1994).  
 CC -!- FUNCTION: PPIases accelerate the folding of proteins. It catalyzes  
 the cis-trans isomerization of proline imidic peptide bonds in  
 oligopeptides.  
 CC -!- CATALYTIC ACTIVITY: Peptidylproline (omega-180) - peptidylproline  
 (omega-0).  
 CC -!- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.  
 CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.  
 CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.  
 CC -----  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: D14073; BAA03158.1; .  
 DR HSSP: P23284; ICYN.  
 DR InterPro: IPR002130; CSA\_PPIase.  
 DR Pfam: PF00160; pro\_isomerase; 1.  
 DR PRINTS: PR00153; CSAPISMRASE.  
 DR PROSITE: PS00170; CSA\_PPIASE\_1; 1.  
 DR PROSITE: PS50072; CSA\_PPIASE\_2; 1.  
 KW Cyclosporin; Isomerase; Rotamase; Signal; Endoplasmic reticulum;  
 KW Multigene family.  
 FT SIGNAL 1 25  
 FT CHAIN 26 208 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B.  
 FT SITE 199 208 PREVENT SECRETION FROM ER.  
 FT CONFLICT 30 30 K -> G (TN REF 3)  
 FT SEQUENCE 208 AA; 22701 MW; 0097C88289AF676 CRC64;  
 SQ  
 Query Match 37.0%; Score 77; DB 1; Length 208;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-63;  
 Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4  
 ID CYPB\_RAT STANDARD; PRT; 208 AA.  
 AC P24368;  
 DT 01-MAR-1992 (Rel. 21, Created)  
 DT 01-MAR-1992 (Rel. 21, Last sequence update)  
 DE 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Peptidyl-prolyl cis-trans isomerase B precursor (EC 5.2.1.8) (PPIase)  
 DE (Rotamase) (Cyclophilin B) (S-cyclophilin) (SCYLP) (CYP-SL).  
 GN PPIB.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 CC NCBI\_Taxid=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=9300692; PubMed=2194066;  
 RA Iwai N., Inagami T.;  
 RT "Molecular cloning of a complementary DNA to rat cyclophilin-like  
 protein mRNA.";  
 RL Kidney Int. 37:1460-1465(1990).  
 RN [2]  
 RP REVISIONS TO C-TERMINUS.  
 RX MEDLINE=92112948; PubMed=1530944;  
 RA Abder S., Krause K.-H., Caroni P.;  
 RT "S-cyclophilin is retained intracellularly via a unique COOH-terminal  
 sequence and colocalizes with the calcium storage protein  
 calreticulin.";  
 RL J. Cell Biol. 116:113-125(1992).  
 CC -!- FUNCTION: PPIases accelerate the folding of proteins. It catalyzes  
 the cis-trans isomerization of proline imidic peptide bonds in  
 oligopeptides.  
 CC -!- CATALYTIC ACTIVITY: Peptidylproline (omega-180) - peptidylproline  
 (omega-0).  
 CC -!- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.  
 CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (By similarity).  
 CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.  
 CC -----  
 CC HSSP: P23284; ICYN.  
 DR InterPro: IPR002130; CSA\_PPIase.  
 DR Pfam: PF00160; pro\_isomerase; 1.  
 DR PRINTS: PR00153; CSAPISMRASE.  
 DR PROSITE: PS00170; CSA\_PPIASE\_1; 1.  
 DR PROSITE: PS50072; CSA\_PPIASE\_2; 1.  
 KW Cyclosporin; Isomerase; Rotamase; Signal; Endoplasmic reticulum;  
 KW Multigene family.  
 FT SIGNAL 1 25  
 FT CHAIN 26 208 BY SIMILARITY.  
 FT SITE 199 208 PREVENT SECRETION FROM ER  
 FT SEQUENCE 208 AA; 23025 MW; 76D12AC3427FEF32 CRC64;  
 SQ  
 Query Match 30.3%; Score 63; DB 1; Length 208;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-50;  
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 89 IKFPMIOGDFTRGDGTGKSIYGERPPDENFKIKHYGGWVSMANAGKDTNGSOPFIT 148  
 DB 89 IKDFMIOGDFTRGDGTGKSIYGERPPDENFKIKHYGGWVSMANAGKDTNGSOPFIT 148  
 OY 149 VKT 151  
 DB 149 VKT 151

RESULT 5  
 ID CYPB\_CHICK STANDARD; PRT; 207 AA.  
 AC P24367;  
 DT 01-MAR-1992 (Rel. 21, Created)  
 DT 01-MAR-1992 (Rel. 21, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)

```

DE Peptidyl-prolyl cis-trans isomerase B precursor (EC 5.2.1.8) (PPIase)
DE (Rotamase) (cyclophilin B) (S-cyclophilin) (SCYLP).
OS Gallus gallus (chicken).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
CC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP MEDLINE=91250364; PubMed=2040593;
RA Caron P., Rothenfluh A., McGlynn E., Schneider C.;
RT "S-cyclophilin. New member of the cyclophilin family associated with
RT the secretory pathway.";
RL J. Biol. Chem. 266:10739-10742(1991).
CC -1- FUNCTION: PPIases accelerate the folding of proteins. It catalyzes
CC the cis-trans isomerization of proline imidic peptide bonds in
CC oligopeptides.
CC -1- CATALYTIC ACTIVITY: Peptidylproline (omega=180) = peptidylproline
CC (omega=0).
CC -1- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (by similarity).
CC -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M63553; AAA49064.1; -.
DR PIR: A40516; A40516.
DR HSSP: P23284; 1CTN.
DR InterPro: IPR002130; CSA_PPIase.
DR Pfam: PF00160; pro_isomerase; 1.
DR PRINTS: PR00153; CSA_PPIASMRASE.
DR PROSITE: PS00170; CSA_PPIASE_1; 1.
DR PROSITE: PS50072; CSA_PPIASE_2; 1.
DR Cyclosporin; isomerase; Rotamase; Signal: Endoplasmic reticulum;
KM Multigene family.
KW SIGNAL
FT SIGNAL 1 24 BY SIMILARITY.
FT CHAIN 25 207 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B.
FT SITE 198 207 PREVENT SECRETION FROM ER
FT (BY SIMILARITY).
FT SEQUENCE 207 AA; 22413 MW; D9C0C2E528E25B59 CRC64;
SQ
Query Match 26.4%; Score 55; DB 1; Length 207;
Best Local Similarity 100.0%; Pred. No. 3.1e-43;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 114 RPDDENFKLKHGPGVSMANACKOTNSQFFITTKTAWLDGKHVFKVLEGM 168
DB 113 RPDDENFKLKHGPGVSMANACKOTNSQFFITTKTAWLDGKHVFKVLEGM 167

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RA Pahl A., Uehlein M., Bang H., Schlumbohm W., Keller U.;
RT "Streptomycetes possess peptidyl-prolyl cis-trans isomerases that
RT strongly resemble cyclophilins from eukaryotic organisms.";
RL Mol. Microbiol. 6:3551-3558(1992).
CC -1- FUNCTION: PPIases accelerate the folding of proteins. It catalyzes
CC the cis-trans isomerization of proline imidic peptide bonds in
CC oligopeptides.
CC -1- CATALYTIC ACTIVITY: Peptidylproline (omega=180) = peptidylproline
CC (omega=0).
CC -1- ENZYME REGULATION: BINDS CYCLOSPORIN A (CSA). CSA MEDIATES SOME
CC OF ITS EFFECTS VIA AN INHIBITORY ACTION ON PPIASE.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
CC -----
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CC -----
DR EMBL: Z15137; CAAT8840.1; -.
DR PIR: S28020; S28020.
DR HSSP: P05092; 2CPL.
DR InterPro: IPR002130; CSA_PPIase.
DR Pfam: PF00160; pro_isomerase; 1.
DR PRINTS: PR00153; CSA_PPIASMRASE.
DR PROSITE: PS00170; CSA_PPIASE_1; 1.
DR PROSITE: PS50072; CSA_PPIASE_2; 1.
DR Cyclosporin; isomerase; Rotamase.
KW SEQUENCE 165 AA; 17716 MW; 2CF1DF725CD6F47D CRC64;
SQ
Query Match 9.1%; Score 19; DB 1; Length 165;
Best Local Similarity 100.0%; Pred. No. 3.2e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 95 QCGDFTRGDTGKSIYGE 113
DB 62 QCGDFTRGDTGKSIYGE 80

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RESULT 6
PPI_STRCH
ID PPI_STRCH STANDARD: PRT; 165 AA.
AC Q06118;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8) (PPIase) (Rotamase)
DE (cyclophilin homolog).
OS Streptomyces chromosomalis.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Streptomycetaceae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1899;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 4-41.
RC STRAIN=ATCC 11523;
RX MEDLINE=93116593; PubMed=1474897;

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RESULT 7
CYP5_CAEEL
ID CYP5_CAEEL STANDARD: PRT; 204 AA.
AC P52013;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Peptidyl-prolyl cis-trans isomerase 5 (EC 5.2.1.8) (PPIase) (Rotamase)
DE (Cyclophilin-5).
GN CYP-5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=96276416; PubMed=8694762;
RA Page A.P., MacIven K., Hengartner M.O.;
RT "Cloning and biochemical characterization of the cyclophilin
RT homologues from the free-living nematode Caenorhabditis elegans.";
RL Biochem. J. 317:179-185(1996).
CC -1- FUNCTION: PPIases accelerate the folding of proteins. It catalyzes
CC the cis-trans isomerization of proline imidic peptide bonds in
CC oligopeptides.
CC -1- CATALYTIC ACTIVITY: Peptidylproline (omega=180) = peptidylproline
CC (omega=0).
CC -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
CC -----
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CC -----  
 DR EMBL: U31948; AAC47126.1; -  
 DR HSSP: P23284; ICYN.  
 DR InterPro: IPR002130; CSA\_PPIase.  
 DR Pfam: PF00160; pro\_isomerase.1.  
 DR PRINTS: PR00153; CSAPISMRASE.  
 DR PROSITE: PS00170; CSA\_PPIASE\_1; 1.  
 DR PROSITE: PS50072; CSA\_PPIASE\_2; 1.  
 KW Isomerase; Rotamase; Multigene family.  
 SQ SEQUENCE 204 AA; 22366 MW; 22ABB39AD1127BAA CRC64;

Query Match 8.2%; Score 17; DB 1; Length 204;  
 Best Local Similarity 100.0%; Pred. No. 2,5e-08;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 91 DFMIOGDFTRGDGTG 107  
 DB 84 DFMIOGDFTRGDGTG 100

RESULT 8  
 CYP6\_CAEEL STANDARD; PRT; 201 AA.  
 ID CYP6\_CAEEL  
 AC P52014;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Peptidyl-prolyl cis-trans isomerase 6 precursor (EC 5.2.1.8) (PPIase)  
 DE (Rotamase) (Cyclophilin-6).  
 GN CYP-6 OR P42G9.2.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peloderae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Bristol N2;  
 RX MEDLINE=96276416; PubMed=8694762;  
 RA Page A.P., MacIiven K., Hengartner M.O.;  
 RT "Cloning and biochemical characterization of the cyclophilin  
 RT homologues from the free-living nematode *Caenorhabditis elegans*.";  
 RL Biochem. J. 317:179-185(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Bristol N2;  
 RA Talc A.;  
 RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: PPIases accelerate the folding of proteins. It catalyzes  
 CC the cis-trans isomerization of proline imidic peptide bonds in  
 CC oligopeptides.  
 CC -1- CATALYTIC ACTIVITY: Peptidylproline (omega-180) - peptidylproline  
 CC (omega-0).  
 CC -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.  
 CC -----  
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CC -----  
 DR EMBL: U27354; AAC67124.1; -  
 DR EMBL: U00051; AAA91355.1; -  
 DR HSSP: P23284; ICYN.  
 DR WormPep: P42G9.2; CE01301.  
 DR InterPro: IPR002130; CSA\_PPIase.  
 DR Pfam: PF00160; pro\_isomerase.1.

DR PRINTS: PR00153; CSAPISMRASE.  
 DR PROSITE: PS00170; CSA\_PPIASE\_1; 1.  
 DR PROSITE: PS50072; CSA\_PPIASE\_2; 1.  
 KW Isomerase; Rotamase; Multigene family; Signal.  
 FT SIGNAL 1 16  
 FT CHAIN 17 201  
 FT CARBOHYD 130 130  
 SQ SEQUENCE 201 AA; 21864 MW; 084C5762917F958B CRC64;

Query Match 7.7%; Score 16; DB 1; Length 201;  
 Best Local Similarity 100.0%; Pred. No. 2,1e-07;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 FMIIOGDFTRGDGTG 107  
 DB 82 FMIIOGDFTRGDGTG 97

RESULT 9  
 CYP\_C\_HUMAN STANDARD; PRT; 212 AA.  
 ID CYP\_C\_HUMAN  
 AC P45877;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Peptidyl-prolyl cis-trans isomerase C (EC 5.2.1.8) (PPIase) (Rotamase)  
 DE (Cyclophilin C).  
 GN PPIC OR CYP.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94304830; PubMed=8031755;  
 RA Schneider H., Charara N., Schmitz R., Wehrli S., Mikol V.,  
 RA Zurini M.G., Quesnau V.F., Moyva N.R.;  
 RT "Human cyclophilin C: primary structure, tissue distribution, and  
 RT determination of binding specificity for cyclosporins";  
 RL Biochemistry 33:8218-8224(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Uterus;  
 RA Strausberg R.;  
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: PPIases accelerate the folding of proteins. It catalyzes  
 CC the cis-trans isomerization of proline imidic peptide bonds in  
 CC oligopeptides.  
 CC -1- CATALYTIC ACTIVITY: Peptidylproline (omega-180) - peptidylproline  
 CC (omega-0).  
 CC -1- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYP.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.  
 CC -----  
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CC -----  
 DR EMBL: S71018; AAB31350.1; -  
 DR EMBL: BC002678; AAH02678.1; -  
 DR HSSP: P05092; 2RMC.  
 DR Genew: HGNC:9256; PPIC.  
 DR MIM: 123842; -  
 DR InterPro: IPR002130; CSA\_PPIase.  
 DR Pfam: PF00160; pro\_isomerase.1.  
 DR PRINTS: PR00153; CSAPISMRASE.  
 DR PROSITE: PS00170; CSA\_PPIASE\_1; 1.  
 DR PROSITE: PS50072; CSA\_PPIASE\_2; 1.  
 KW Cyclosporin; Isomerase; Rotamase; Multigene family.

SEQ SEQUENCE 212 AA; 22763 MW; 6F3DB547A2AE581B CRC64;

## Query Match

Best Local Similarity 7.7%; Score 16; DB 1; Length 212;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 83 SKFHRYKDFMIOGCD 98  
|||||  
DB 85 SKFHRYKDFMIOGCD 100

## RESULT 10

CYPC\_MOUSE

ID CYPC\_MOUSE STANDARD: PRT: 212 AA.

AC P30412:

DT 01-APR-1993 (Rel. 25, Created)

DT 01-APR-1993 (Rel. 25, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Peptidyl-prolyl cis-trans isomerase C (EC 5.2.1.8) (PPIase) (Rotamase)

DE (Cyclophilin C).

GN (Cyclophilin C).

GN PPIase OR CYPC.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP MEDLINE=91347379; PubMed=1552374;

RX Friedman J., Weissman I.L.;

RT "Two cytoplasmic candidates for immunophilin action are revealed by

RT affinity for a new cyclophilin: one in the presence and one in the

RT absence of GsA.";

RL Cell 66:799-806(1991).

CC -1- FUNCTION: PPIases accelerate the folding of proteins. It catalyzes

CC the cis-trans isomerization of proline imidic peptide bonds in

CC oligopeptides.

CC -1- CATALYTIC ACTIVITY: Peptidylproline (omega=180) -&gt; peptidylproline

CC (omega=0).

CC -1- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPC.

CC -1- SURCELLULAR LOCATION: Cytoplasmic.

CC -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.

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CC -----

CC EMBL: M74227; AAA37511.1; -

CC PIR: A40047; A40047.

CC HSSP: P05092; 2RMC.

CC MGD: MG1:97751; PPIc.

CC InterPro: IPR002130; CSA\_PPIase.

CC Pfam: PF00160; pro\_isomerase; 1.

CC PRINTS: PR00153; CSA\_PPIASE.

CC PROSITE: PS00170; CSA\_PPIASE\_1; 1.

CC PROSITE: PS50072; CSA\_PPIASE\_2; 1.

CC CYCLOSPORIN: Isomerase; Rotamase; Multigene family.

CC KW CYCLOSPORIN: Isomerase; Rotamase; Multigene family.

CC SQ SEQUENCE 212 AA; 22794 MW; C99E7A5D0FA04B6 CRC64;

OY 85 FHRVINDFMIOGCDFT 100

DB 87 FHRVINDFMIOGCDFT 102

RESULT 11  
CYP7\_CAEBL

ID CYP7\_CAEBL STANDARD: PRT: 171 AA.

AC P52015:

DT 01-OCT-1996 (Rel. 34, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Peptidyl-prolyl cis-trans isomerase 7 (EC 5.2.1.8) (PPIase) (Rotamase)

DE (Cyclophilin-7).

DE CYP-7 OR Y75B12B.2.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;

OC Rhabditidae; Peloderinae; Caenorhabditis.

OX NCBI\_TaxID=62319;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-Bristol N2;

RX MEDLINE=96276416; PubMed=8694762;

RX Page A.P., Macniven K., Hengartner M.O.;

RT "Cloning and biochemical characterization of the cyclophilin

RT homologues from the free-living nematode *Caenorhabditis elegans*."

RT Biochem. J. 317:179-185(1996).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-Bristol N2;

RX White S.;

RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE OF 1-13.

RC STRAIN-Bristol N2;

RX MEDLINE=97295299; PubMed=9150941;

RX Binl L., Held H., Liberatori S., Geler G., Pallini V., Zwilling R.;

RT "Two-dimensional gel electrophoresis of *Caenorhabditis elegans*

RT homogenates and identification of protein spots by microsequencing."

RT Electrophoresis 18:557-562(1997).

RL Electroforests 18:557-562(1997).

CC -1- FUNCTION: PPIases accelerate the folding of proteins. It catalyzes

CC the cis-trans isomerization of proline imidic peptide bonds in

CC oligopeptides.

CC -1- CATALYTIC ACTIVITY: Peptidylproline (omega=180) -&gt; peptidylproline

CC (omega=0).

CC -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.

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CC -----

CC EMBL: U27559; AAC47125.1; -

CC EMBL: AL032663; CAA21760.1; -

CC HSSP: P05092; 1CWL.

CC Sienna-2DPAGE; P52015; -

CC WormPep: Y75B12B.2; CE20371.

CC InterPro: IPR002130; CSA\_PPIase.

CC Pfam: PF00160; pro\_isomerase; 1.

CC PRINTS: PR00153; CSA\_PPIASE.

CC PROSITE: PS00170; CSA\_PPIASE\_1; 1.

CC PROSITE: PS50072; CSA\_PPIASE\_2; 1.

CC Isomerase; Rotamase; Multigene family.

CC KW Isomerase; Rotamase; Multigene family.

CC FT CONFLICT 12 12 I -&gt; T (IN REF. 1).

CC SQ SEQUENCE 171 AA; 18401 MW; D5BDS32A32942A7 CRC64;

RESULT 12  
CYPB\_CAEBL

Query Match 7.2%; Score 15; DB 1; Length 171;  
Best Local Similarity 100.0%; Pred. No. 1.5e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 148 TVKTAWLDGKHVYFG 162  
|||||  
DB 123 TVKTAWLDGKHVYFG 137

ID CYPB\_CAEEL STANDARD: PRT: 183 AA.  
AC P52018;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Peptidyl-prolyl cis-trans isomerase 11 (EC 5.2.1.8) (PPIase)  
DE (Rotamase) (Cyclophilin-11).  
GN CYP-11 OR T01B7.4.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Peleoderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC SRRATN-Bristol N2;  
RX MEDLINE=96276416; PubMed=8694762;  
RA Page A.P., Macniven K., Hengartner M.O.;  
RT Cloning and biochemical characterization of the cyclophilin  
RT homologues from the free-living nematode *Caenorhabditis elegans*.  
RL Biochem. J. 317:179-185(1996).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC SRRATN-Bristol N2;  
RX Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: PPIases accelerate the folding of proteins. It catalyzes  
CC the cis-trans isomerization of proline imidic peptide bonds in  
CC oligopeptides.  
CC -1- CATALYTIC ACTIVITY: Peptidylproline (omega-180) - peptidylproline  
CC (omega-0).  
CC -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL: U34955; AAC47115.1; -  
CC EMBL: Z66499; CAA91297.1; -  
CC HSSP: P05092; 2CPL.  
CC WormRep: T01B7.4; CE03588.  
CC InterPro: IPR002130; CSA\_PPIase.  
CC Pfam: PF00160; pro\_isomerase; 1.  
CC PRINTS: PR00153; CSAPISMRASE.  
CC PROSITE: PS00170; CSA\_PPIASE.1; 1.  
CC PROSITE: PS50072; CSA\_PPIASE.2; 1.  
CC Isomerase; Rotamase; Multigene family.  
CC KW SEQUENCE 183 AA; 20193 MW; 23549C922828C533 CRC64;  
SQ  
Query Match 7.2%; Score 15; DB 1; Length 183;  
Best Local Similarity 100.0%; Pred. No. 1.6e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 85 FHRVINDFMIOGDF 99  
Db 71 FHRVINDFMIOGDF 85

RESULT 13  
PPIB\_TREPA  
ID CYPB\_TREPA STANDARD: PRT: 215 AA.  
AC O66105;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Probable peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8) (PPIase)  
DE (Rotamase).  
GN PPIB OR PPI OR TP0947.  
OS *Treponema pallidum*.  
OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.

OX NCBI\_TaxID=160;  
RN [1]  
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RX MEDLINE=97461344; PubMed=9317025;  
RA Shevchenko D.V., Atkins D.R., Robinson E.J., Li M., Shevchenko O.V.,  
RA Rodolfo J.D.;  
RT Identification of homologs for thioredoxin, peptidyl prolyl cis-trans  
RT isomerase, and glycerophosphodiester phosphodiesterase in outer  
RT membrane fractions from *Treponema pallidum*, the syphilis spirochete.  
RL Infect. Immun. 65:4179-4189(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC SRRATN-Nichols;  
RX MEDLINE=98332770; PubMed=9665876;  
RA Fraser C.M., Norris S.J., Weinstein G.M., White O., Sutton G.G.,  
RA Dodson R., Gwin M., Hickey E.K., Clayton R., Ketchum K.A.,  
RA Sodergren E., Hardham J.M., McLeod M.P., Salberg S., Peterson J.,  
RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Uterback T.,  
RA McDonald L., Arlath P., Bowman C., Cotton M.D., Fujii C., Garland S.,  
RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,  
RA Venter J.C.;  
RT Complete genome sequence of *Treponema pallidum*, the syphilis  
RT spirochete.  
RL Science 281:375-388(1998).  
CC -1- FUNCTION: PPIases accelerate the folding of proteins. It catalyzes  
CC the cis-trans isomerization of proline imidic peptide bonds in  
CC oligopeptides (By similarity).  
CC -1- CATALYTIC ACTIVITY: Peptidylproline (omega-180) - peptidylproline  
CC (omega-0).  
CC -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.  
CC  
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CC  
CC EMBL: U97573; AAC08055.1; -  
CC EMBL: AE001263; AAC65904.1; -  
CC HSSP: P05092; 2RMC.  
CC TIGR: TP0947;  
CC InterPro: IPR002130; CSA\_PPIase.  
CC Pfam: PF00160; pro\_isomerase; 1.  
CC PRINTS: PR00153; CSAPISMRASE.  
CC PROSITE: PS00170; CSA\_PPIASE.1; 1.  
CC PROSITE: PS50072; CSA\_PPIASE.2; 1.  
CC Isomerase; Rotamase; Complete proteome.  
CC KW SEQUENCE 215 AA; 23272 MW; CCA1589C1F5A6D0B CRC64;  
SQ  
Query Match 6.7%; Score 14; DB 1; Length 215;  
Best Local Similarity 100.0%; Pred. No. 1.5e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 85 FHRVINDFMIOGDF 98  
Db 89 FHRVINDFMIOGDF 102

RESULT 14  
CYPH\_ALICE  
ID CYPH\_ALICE STANDARD: PRT: 150 AA.  
AC P34887;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8) (PPIase) (Rotamase)  
DE (Cyclophilin) (Cyclosporin A-binding protein).  
GN CYP.  
OS *Allium cepa* (onion).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Alliaceae;

